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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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                        /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn~emb1/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (without alignments)
10417.308 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	Length	DB	ID	Description
1	2151	100.0	2151	20	AAX86501	cDNA encoding a hu
2	2151	100.0	2151	21	AAA51229	Human beta-TrCP co
ω	2151	100.0	2151	21	AAZ93350	Sequence encoding
4	2151	100.0	2151	21	AAZ93710	F -box protein hBe
ر ن	2151	100.0	2151	22	AAC84610	Human ZF11 protein
6	2120.8	98.6	3220	22	ААН90079	Human bone marrow
7	2114.8	98.3	2419	21	AAZ29233	Human cell signall
8	2011.4	93.5	3622	22	AAH89966	Human bone marrow
9	2008.2	93.4	3003	22	AAK52699	Human polynucieoti

29-JAN-1999; 05-AUG-1999.

99WO-FR00196

Probe #15982 used t	AAI47296 AAI07701	22	370 370		208.4 208.4	44	0.0	
#11938	AAI22005	22	370	9.7	208.4	43	C	
bone ma	AAK41254	22	370		208.4	42	C	
Human brain expres	AAK15524	22	370		208.4	41	O	
æ	ABA34172	22	370	9.7	208.4	40	a	
Human foetal liver	ABA67080	22	370	9.7	208.4	39	C	
•	ABA49167	22	370	9.7	208.4	38	ဂ	
Human genome-deriv	ABS02776	24	479	12.6	272	37	a	
Probe #2737 used t	AAI02746	22	479	12.6	272	36	O	
used	AAI34184	22	479	12.6	272	35	O	
2761 tor 9	AAI12828	22	479	12.6	272	34	C	
	AAK28263	22	479	12.6	~	<u>ω</u>	ဂ	
Human brain expres	AAK02821	22	479	12.6	7	32	C	
	ABA24312	22	479	12.6	272	31	ი	
	ABA54530	22	479	12.6	7	30	a	
	ABA44075	22	479	12.6	7	29	C	
Drosophila melanog	ABL06080	23	9129		288	28	O	
Human prostate exp	ABV58856	23	594		387.6	27		
cDNA encoding huma	ABK43155	23	951		435.4	26		
Beta-TRCP.N/SKP2.C	AAC84601	22	1561		518.8	25		
Differentiation In	AAZ09025	20	647		572.6	24		
Human beta TrCP (b	ABK86903	24	657	30.5	657	23		
Drosophila melano	ABL06081	23	2387		676.4	22		
Human polynucleoti	AAI59364	22	4360		•	21		
Human polynucleoti	AAK52260	22	4344	41.1	883.4	20		
Human E3 ubiquitin	AAA51228	21	4230		883.4	19		
Human polynucleoti	AA161150	22	2084	41.1	883.4	18		
Mouse ubiquitin li	AAA73131	21	1707	7.	1443	17		
F-box protein FWD1	AAZ93714	21	2175	œ	1682.2	16		
Human polynucleot	AAK51716	22	2207	8	1688.8	15		
Human polynucleoti	AAK51717	22	2366		1697.8	14		
Human polynucleoti	AAK51715	22	2285	80	1697.8	13		
Human beta-transdu	AAA73132	21	1707		1707	12		
Human polynucleot	AAK52701	22	3003	93.4	2008.2	11		
Human polynucleoti	AAK52700	22	3003	93.4	2008.2	10		

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
AAX86501
Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-catenin; proteosome deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation;
                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                             cDNA encoding a human beta-transducin repeat containing protein
                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX86501 standard; cDNA; 2151 BP.
                                                                                                                                                                                                                                                                                                                                                                                                         AAX86501;
                                                                         W09938969-A1
                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                         tumour necrosis factor; ss.
                                                                                                                                                 Location/Qualifiers 70..1779
                                                                                                    /note= "beta-transducin repeat containing protein"
                                                                                                                     /product= beta-TrcP
                                                                                                                                     /*tag=
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The present sequence encodes a human beta-transducin repeat containing CC protein (beta-Trcp). The protein directs proteins to the proteosome CC degradation pathways. The protein is able to interact with the Vpu CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins CC likappaB or beta-catenin (bc) and/or protein Skpip. The protein controls CC ubiquitinylation of phosphorylated proteins and thus their targeting to CC proteosomes for degradation. Depending on whether the process is CC inhibited or promoted, the result may be delayed breakdown of CD4 (in CC cases of HIV-1 infection), increased activity of IkB (and thus reduced CC activity of NrkappaB) and increased activity of mutant bC in tumour CC cells, or increased bC survival (and reduced apoptosis) in Alzheimer's CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals), CC antitumour agents that disrupt cells, and anti-inflammatory agents that CC disrupt activation by NrkappaB. Fragments of the protein are also CC second antivariation or accute inflammation or accute inflammatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 2151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         associated with release of tumour necrosis factor.
                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumour, anti-inflammatory and anti-Alzheimer's agents
                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                  181
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30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA
                                                 AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAAGTGGAATTTGTG
                                                                            AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
                                                                                                                                                GGCACTTCCAGTATGATTGTGCCCAAGCAACCGGAAACTCTCAGCAAGCTATGAAAAGGAA
                                                                                                                                                                          GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA 360
                                                                                                                                                                                                                                                   TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAAT
                                                                                                                                                                                                                                                                                                AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTA
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                                                                                                                                                                                                                                                                                                                                                  AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTA
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Margottin F;
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98FR-0001100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2151; 100.0%; Pred. No. 0;
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TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGGATCTT
                                                        GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
                                                                         GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
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                                                                                                                                                                                                                                             Human beta-TrCP coding sequence
                                                                                                                                                                                                                                                                                                                  AAA51229 standard;
                                                                                                   WO200034447-A2
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                                        CATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACAT 1680
                                                                                GTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG
                                                                                                                                                                                  TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT
                                                                                                                                                                                                                                            GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
                                                                                                                                                                                                                                                                                                                          TACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATA
                                                                                                                                                                                                                                                                                                                                                                                                       TTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACA 1320
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                                                                       28-AUG-1998;
03-FEB-1999;
15-MAR-1999;
WPI; 200
P-PSDB;
                                                                                                                                                                                                                                  Homo
                               Chiaur DS,
                                                                                                                27-AUG-1999;
                                                                                                                                                                                                                                                            antagonist; proliferative disorder; differentiative disorder; breast cancer; prostate cancer; ovarian cancer; cancer; small cell lung carcinoma; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                           F-box protein; FBP; diagnosis; treatment; screening; agonist;
                                                                                                                                                                                                                                                                                                                                                                                AAZ93350 standard; cDNA;
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                                                  (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                     09-MAR-2000.
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                                                                                                                                                                                                                                                      inflammatory disorder; human; ss.
                                                                                                                                                                                                                                                                                                                  Sequence encoding F-box protein FBP-1.
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                            Pagano M,
                                                                                                                                                                                                                                                                                                                                       (first entry)
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99US-0118568.
99US-0124449.
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                                                                                                                                                                                       Location/Qualifiers 70..1779 /*tag= a
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 2151; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast, ovarian and prostate cancer and small cell lung carcinoma and also major opportunistic infections, immune disorders, cardiovascular diseases and inflammatory disorders. FBP protein, analogs, derivatives and their subsequences, anti-FBP antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FBP gene expression. Cells expressing such proteins or their fragments are useful for screening compounds. The compounds are agonists or antagonists, which are useful for treating a proliferative or differentiative disorder in a mammal such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases with F-box motifs (F-box proteins) are useful for diagnosis of proliferative and differentiated related disorders by measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                  CCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCT
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                                                                                                                                                                                                                     GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAG
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2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;
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Pred. No. 0;
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D 04	7	81 AAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAGACATAGTTTA 8 	0 0
γΩ	œ	1 CAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT	
П	80	41 CAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGAT	00
n		01 CAGAAAATAGTAAGCGGCCTTCGAGACACACACACTCAAGATCTGGGATAAAAACACACATTG 9	
ы	Db 9	AGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAAACACAA	0
, n	0 9	61 GAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAG 1	020
2		GAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAGG	.080
п	10	21 AGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAGGT 1	080
_	10	AAATGCTAAACACGTTGATTCACCATTGTGAAGCAGT	
) 10	CTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAA1	1140
	: =	41 GGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA 1	200
_		T GGCUIGUIGGIGUCCIGCICCHRUMITCGIICCHIIGCIGIA	
~	ь	1 ACTGACATTACCCTCCGGAGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC	26
н	Д	01 ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC	26
_	Qy 12	61 TTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACA	w
-	12	61 TTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACAC	1320
_	13	21 ACTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAG 1	1380
_	13	21 AGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGC	1380
_	Qу 13	81 TACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATA 1	1440
		81 TACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACAT	1440
_	0у 14	41 GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCCATGAGGAATTGGTGCGTTGTATTCGA 1	1500
	<u> </u>	41 GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCG	1500
	Оу 15	01 TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTT	1560
_		01 TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGG	1560
_	Qу 15	61 GTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG	1620
	Db 15	61 GTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAG	1620
_	Оу 16	21 CATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACAT	1680
_	-	21 CATTCCGGAAGAGTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACAT	1680
_	Qy 16	81 GATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCC	1740
_	<u></u>	81 GATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCCAAGCTGAACCCCCC	1740
_	Qy 17	41 CGTTCCCCTTCTCGAACATACACCTACATCTCCAGATAAATAA	1800
	77. qa	41 CGTTCCCCTTCTCGAACATACACCTACATCTCCAGATAAATAA	1800

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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of
                                                                                                             Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with uniquitin protein ligase or inhibiting ubiquitination using organic
                                                                       Claim 10; Page 171; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the method are approximated to the provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the
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                                        The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUI-1 (a member of the cullin/CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDA2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
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                                                                                                                                                                                                               Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
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P-PSDB; AAB48298.
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Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T;
                             treating tumours.
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                                                                                                                                                                                                                         immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coaquiation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                              The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various polypeptide encoded by it are useful in the treatment of various polypeptide encoded by it are useful in the treatment of various polynemia.
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{\tt TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAAT}
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2419 BP; 671 A; 531 C; 625 G; 590 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                disorders like AIDS, Addison's disease, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9;
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GCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCCA 310
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                                                                                                                               GAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTTA
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                                                                                                                                                                                              TGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAATTCCTCAGAGA
                                                                                                                                                                                                                 TGGACCCGGCCGAGGCGGTGCTGCAAGAGAGAGCCACTCAAGTTTATGAATTCCTCAGAGA 130
                                                                                                                                                                                                                                                              GGGGCCTGGCACCAAAGGGGCGGCCCCGGCGGAGAGCGGACCCAGTGGCCTCGGCGATTA 70
                                                                                                                                                                                                                                                                                               GCGGCCTGGCACCAAAGGGGCGGCCCCGGCGAGAGCGGACCCAGTGGCCTCGGCGATTA 70
                                                               GACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCAA
                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                               Conservative
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/product= "Cell Signalling Protein-12"
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Best Local Similarity 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alabeimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000US-0488725
25-JAN-2000; 2000US-0552317
09-JUL-2000; 2000US-0598042
19-JUL-2000; 2000US-0620312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 274-275; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3622 BP; 961 A; 839 C; 874 G; 948 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
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                                                                                                                                                                                                                                                                                                               172 CCAGAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 231
 472 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT
                                  561
                                                                                                                                                                441 CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
                                                                                                                                                                                                                                                                                                                                                           261 TTCCAGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 320
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                                                 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                                 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
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                                                                                                                                                                               CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
                                                                                                                                                                                                                             GAAACAGTATGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAA 291
                                                                                                                                                                                                                                                                                              CCAGAGAAGTTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA
                                  GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
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Zhou P,
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2000US-0598042
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u C, Xue AJ, Yang
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ARATCTEMAACCTACGTGGAGGGATTCATTAACTGCTGCGAACCCAATCCACTACTCGGGATTGGT. ARATCGCTGGAGAACCTTCTGCCATACCTGGTGGAATCACTACTCGCGGATTGGT. ARATCGCTGGAGAACCTTCTGCCATACCTGGATGCCAATCACTATGCCTGGCTGAACTT. TGTGCAAGGAATGGTACCGAGTGACCTCTGATGCCTGGATGGA	55	64	49	58	52	37	31 46	4	25	.34	.19	.28	13			<u> </u>	1012	0	Ū	4	9	œ	ω	N	7	9	<u> —</u>	0	Ü	4	9		ū	N
	TGGGATCTTGTGGCTGCTTTGGACCCCCGGTGCTCCTGCAGGGACACTCTGTCTACGGACC 1	GTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTG	GTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCCTATGATAGAAAATTAAAAGTG 1	GGGACATAGAATGTGGTGCATGTTTACGAGTTTAGAAGGCCATGAGGAATTGGTGCGT 1 		GTTTGCAGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTA 1	GGANCACANGTACTTGTGAATTTGTAAGGACCTTAAATGGACNCAAACGAGGCATTGCC 1 1 1 1 1 1 1 1 1 1	TTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTA 1	TTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTA 1	CCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAAT 1	CCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAAT 1		TCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATG 1	TACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGT 1	TACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGT 1		ATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTA 1		CACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG 1		ATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA 9		ATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG 8		TTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA 8	ATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTATAGAGGCA	ATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCA 7	GAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAG 8	GAATGGTCAGGACAGATTCTCTGTGGGAGAGGGCCTGGCAGAACGAAGAGGATGGGGACAG 7	TGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG	TGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG 6	ATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT 7	ATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT 5	

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                                                                       19-JUL-2000;
01-SEP-2000;
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20-OCT-2000;
30-NOV-2000;
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27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                           (HYSE-)
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                                                                       2000US-0496914
2000US-0560875
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2000US-0728422
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or reatment of carnot landscaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
Zhao QA,
Xue AJ,
                            Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                             inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-476283/51.
                                                                                                                                                                                                                                                                                                                        Page 4584-4585; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Cher
Wejhrman T, Goodrich R;
                                          the relevant pages from the sequence listing
                                                                2111 (AAK52582) and 3666
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Chen R, Wang
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Matches Query Match Sequence 3003 BP; 807 A; 703 C; 721 G; 772 T; 0 other; Local 2024; Similarity Conservative 93.48; 0; Mismatches Score 2008.2; Pred. No. 0; DB 22; Length 3003; 80 Indels 1; Gaps ۲,

뫄 Вþ QΥ 밁 Ş Qy В 멍 Ş В δ В Qy B δÃ 맑 Ş ᄝ Q 472 538 598 478 292 298 | GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG CATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGCAACTT TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT AGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAG GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG CATATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTGCCAGCTCGGGGATTGGAT GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT 837 651 591 717 531 471 411 537 477 291 657 597 351

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   TGACCTCATACTTGCCCAGGACCCATTAAAG-TTGCCGTATTTAACGTATCTGCCAATAC
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30-NOV-2000;
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27-APR-2000;
20-JUN-2000;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                             Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                    vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                            Claim 1; Page 4585-4586;
                                                                Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy - \,
                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098
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DB; AAM79567.
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                                                                                                                                 Wang D, Wang J,
Yang Y, Wejhrman
                                                                                                                                                      Liu C, Drmanac RT,
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2000US-0654936.
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  1078
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TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA
                     TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA
                                                                             CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
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ACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAGATGTCTTCTATCAATTGTGAA 20 	AGCAGGGCTTTGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCGGCCCAGGACGGTCT 19	CAGGATGAGCAACAACAGTAACAATCAAACTACTGCCCAGTTTCCCCTGGACTAGCCGAGG 1 	TGACCTCATACTTGCCCAGGACCCATTAAAG-TTGCGGTATTTAACGTATCTGCCAATAC 1 	GAACCCCCCGTTCCCCTTCTCGAACATACACCTACATCTCCAGATAAATAA	AGTTCACATGATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGGCCAAGCT 17 	CTTGTGGAGCATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGT 16 	TGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACC 16 	TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTG 15 	TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGT 14 	TGTTTGCAGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTA 14 	TGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCC 13 	GTTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTA 13 	GCCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAAT 12	TTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATG 11 	AATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGT 11 	TATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTA 1 	AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG 10
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Query Match
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-062325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-OCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM5323-AAM63032) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
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                                                                Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                  activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                  Sequence 3003 BP; 807 A; 703 C; 721 G; 772 T; 0 other;
                                                                                                                                                                                                                                                                                                                           Claim 1; Page 4586-4587; 6221pp; English.
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                                                                                                                    inflammation
                                                                                                                                  treatment of cancer, leukaemia, nervous system disorders, arthritis and
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DB; AAM79568.
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Score 2008.2;
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112 TITANGAATTCCTCGGGGGGAGAGAGCTGTAATAATGGGGAACCCCCTAGGAACTATATATGCGGAACCTCTAATATATGCCCAAACCCCCTAGGAACTATATATGCCCCAAACCCAACCCCCTAGGAACACTAATATATGCCCAAACCCAA	Qy	Ωу	рь	. B &	ם ט	Ag qq	Qy Db	Qy Oy	Qy	Db Qy	Db Qy	Дy	B 64	ag Qy	Db Qy	Ωу	dd VQ	Qy	ДЬ	• •
TTTATGAATTCCTCAGAGAGAGACACTGTAATAATGCCGAACCCCCTAGAAGATATATTCCAAGATTCTTTTATAGAGAGATTCATTATCCAGAGATTCCTCAGAGAGAACACCCCTAGGAAGATATTATTCCAGAGAATTCCTCAGAGAGACACTCCTTCAGAGACACCAACCA	13	25	119	13	07	101	95 83	89 77	712	83	59 77	53 71	47 65	41 59	53 53	29 47	23 41	17 35	N 1-1	Best Lo Matches
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                                                               TGATTGGAACTTTTAAACCTCCCCTCCTCCTCCTTTCACCTCTGGCACCTAGTTTTTTC
                                                                                                                 ACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAAGATGTCTTCTATCAATTGTGAA
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CCATTGGTTCCAGACAAAGGTGACTTATAAATATATTTAGTGTTTTGCCAGAA 2330
                                                   TGATTGGAACTTTTAAACCTCCCCTCCTCCTCCTCCTTTCACCTCTGCACCTAGTTTTTTC
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RESULT 12
AAA73132
ID AAA73132 standard; cDNA; 1707 BP
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AC AAA73132;
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Query Match Matches 1707; The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein. Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used to the gene therapy of colon cancer by being recombined to a virus vector. The present sequence encodes the human beta-TrCP protein from the Sequence 1707 BP; 514 A; 349 C; 414 G; 430 T; 0 other; Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skp1; Cull; F-box motif; WD40 repeat motif; FWD1; gene therapy; colon cancer; beta-transducin repeat containing protein; beta-TrCP; ss. Disclosure; Fig 17; 19pp; Japanese. F-box protein of ubiquitin ligase SCF complex which promotes ubiquitination of IkappaB or beta-catenin -02-DEC-1998; 20-JUN-2000 JP2000166542-A Homo sapiens (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN 27-NOV-2000 (first entry) Local Similarity 2000-485550/43. beta-transducin repeat containing protein (beta-TrCP) cDNA invention. Conservative 98JP-0343437 79.4%; 0 Score 1707; Pred. No. 0; Mismatches 띪 21; 0; Indels Length 1707; 0; the Gaps for 0;

Q Ş 밁 δÃ В 뫄 Q B δÃ 멁 20 밁 Qy 430 301 241 310 181 121 190 130 250 61 70 ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAGAGCACTCAAGTTTATGAATTCCTCAGAG 129 TGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTTGTGGGAACATCTT AGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAACTTGCCAATGGCACTTCC AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 189 ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG AGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCC AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAATTCCTCAGAG 489 369 249 360 300 309 180 120 60 240

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                                                                       AAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCT 1569
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27-APR-2000; 2000US-0560875.

20-JUN-2000; 2000US-0598075.

19-JUL-2000; 2000US-0620325.

01-SEP-2000; 2000US-0654936.

15-SEP-2000; 2000US-0663561.

20-CCT-2000; 2000US-0693325.

30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                  Tang YT,
Zhao QA,
Xue AJ,
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                       Claim 1; Page 1177-1180; 6221pp; English.
                                                                                                                                                                                                                          useful in diagnosis and gene therapy
                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                    WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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Yang Y, Wejhrman T,
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Zhang J, Ren F, Chen
T, Goodrich R;
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                                                                                                   TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA
                                                                                                                                             CATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAG
                                                                                                                                                                        CTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA 831
                                                                                                                                                                                                                                                                                 TATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCA
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TATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTA 1071
                             ACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG
                                            AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAG 1011
                                                                                     TATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAA
                                                                                                                                                                                                       CTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA
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TGACCTCATACTTGCCCAGGTATCGAAATCGATTATGTACATAAC
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RESULT 14
AAK51717
AAK51717 standard;
cDNA; 2366
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ВP

Human polynucleotide SEQ ID

NO 262

06-NOV-2001

(first entry)

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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humnomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss. Homo sapiens

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Best Local
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19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM/8323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer leukamia persona evertem discretaes artheric and
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2366 BP; 661 A; 519 C; 594 G; 592 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 1183-1186; 6221pp; English.
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P-PSDB; AAM78584.
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              GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG 471
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 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
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                                                                                                                                                                                                                                                                                                                                       Conservative
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99.0%;
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Pred. No. 0;
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20-JUN-2000;
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01-SEP-2000;
The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities,
                                                                   Claim 1; Page 1180-1183; 6221pp; English.
                                                                                                 Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
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Wejhrman T,
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e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity activin/inhibin activity and may be useful in the diagnosis and/or
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Search completed: February 21, 2003, 22:17:15 Job time : 484 secs

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BM542586 AGENCOURT	BM54258	_	1081	9	1	43	
вм214360 С0849Е05-	BM21436		656	9	16	42	
BI278543 UI-R-CW0-	BI27854	_	642	9	17.	41	
C0800D04	BM211	1	664	9.	19.	40	
BQ340149 QV2-NN200	BQ34014	1,	509	9.	٠	39	
md93a04.y	AI430490	9	506	0	38.	38	
BQ383756 NISC_mn03	BQ383	1	621	0.	38.	37	
60109924	BE28406	1	577	0.	4	36	
AV716543 AV716543	AV71654		717	0	43.	35	
AA478504 zw95b10.r	AA4785	9	553	0.	44.	34	
BQ211349 UI-R-DY1-	BQ211	1	666	0.	45.	33	
BE109603 UI-R-BJ1-	BE10960	ĭ	682	0	5	32	
AI073856 oo11d08.x	AI073856	9	464	۲.	٠	31	
BM214068 C0845E10-	BM214	1	695	۳.	56.	30	
вJ048898 вJ048898	вJ04889	H	704	٠,	58.	29	
AL642623	AL642623	9	665		59.	28	
AGENCO	BQ940	1	972	۲.	64.	27	
DKFZp686	AL707470	9	656	۲.	46	26	
BF781002 602106631	BF78100	1.	658		71.	25	
6028527	B1088	<u>_</u>	732		72.	24	
) ux60f06	BG27774	۲.	580	2	ω.	23	
AL556068	AL556068	9	945	2.	83.	22	
225612	BF07612	Ľ	521	2	83.	21	
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UI-M-FIO	BQ77110	1,	850	ω ·	49	18	
BG082149 H3073A06-	2 в 6082149	12	646	23.3	500.4	17	
UI-M-EHO	BM94430	1,	810	4.	16.	16	
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DKF2p434D	AL041438	9	544		29.	14	
BI103092 602889321	в110309		637	٠	32 •	13	
BG518761 602578346	BG51876		789	4	34.	12	
BG722472 602693716	BG72247	1	752		66.	11	
BG829037 602753364	BG82903	1	743	7.	80.	10	
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BE269297 601186356	BE26929	1(692	œ	08.	7	

ALIGNMENTS

5 =	Score	Query Match	Query Query Match Length DB ID	DB	ID	Description
_	650.6 30.2 709	30.2	709	12	12 BE782628	BE782628 601465751
N	638	29.7	778	14	BQ444188	BQ444188 UI-M-EX0-
ω	635.2	29.5	652	9	AL044095	AL044095 DKFZp434M
4	625	29.1	851	14	BQ425358	BQ425358 AGENCOURT
տ	624.8	29.0	973	13	BM465280	BM465280 AGENCOURT
σ	613.2	28.5	758	10	BE296484	BE296484 601174756

FEATURES SOUTCE	COMMENT	JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	LOCUS DEFINITION	RESULT 1 BE782628
Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9617 row: f column: 13 High quality sequence stop: 655. Location/Qualifiers 1709	Contact: Robert Strausberg, Ph.D.	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 709)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BE782628.1 GI:10203826	mRNA sequence. BE782628	BE782628 709 bp mRNA linear EST 20-OCT-2000 601465751F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868812 5',	

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VERSION
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ORIGIN
                         ACCESSION
                                                                      DEFINITION
                                                                                                                   BQ444188
                                                                                                                                        RESULT 2
                                                                                                                                                                                                                                                   1882 ACTGCCCAGTTTCCCTGGACTAGCCGAGGAGCAGGGCTTTGAGACTCCTGTTG 1934
                                                                                                                                                                                                                                                                                                                       1822 GTTGCGGTATTTAACGTATCTGCCAATACCAGGATGAGCAACAACAACAATCAAACT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                            1762 ACCTACATCTCCAGATAAATAACCATACACTGACCTCATACTTGCCCAGGACCCATTAAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1702 GACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCCGTTCCCCCTTCTCGAACATAC 1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1642 CTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACAATCCTCATCTGG 1701
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                                                                                                                                                                                                      AGTGGCCAGTTTCCCTGGACTAACCGAGGAGCCAGCGTTGGAGACTCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGGATAGTC
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                                                                                                                                                                                                                                                                                               GTTGCGGTA-TTAACGTATCTGCCAATACCAGGATGAGCAACAACAGTAACAATC-AACT
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                         BQ444188
                                                             UI-M-EX0-bxj-1-06-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone
                                                                                            BQ444188
                                               IMAGE:5709077 5', mRNA sequence
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3868812"
/clone_lib="NIH_MGC_67"
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SOURCE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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436 CAAATGTGTCATTACCAACATGGGCACATAAAACTCGTATCTTAAACCTATGTTGCAGAGA 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 GCTATGAAGACTGAGAATTGTGTGGCCAAAACAAACTTGCCAATGGCACTTCCAGTATG 315
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GATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATTCTGTCA 555
                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTTATATCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTGTGTGTC 375
                                                                                                                                                                                                             Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: pYX-5
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//dev_stage="embryo 15.5 dpc"
//lab_host="DHIOB ([1] phage resistant)"
//lab_host="DHIOB ([1] phage resistant)
//lab_host="DHIOB ([1
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/db_xref="taxon:10090"
/clone="IMAGE:5709077"
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dKfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 bp mRNA linear EST 29-FE: DKFZp434M1528_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M1528 5', mRNA sequence.
                                                                                                                                                     Berlin-Charlottenburg, GERMANY;
                                                                                                                                                                    Please contact the RZPD:
                                                                                                                                                                                 This clone (DKFZp434M1528) is available at the RZPD in
                                                                                                                                                                                                   No s1 sequence available
                                                                                                                                                                                                                   German Genome Project
                                                                                                                                                                                                                                                                                                                                          Contact: Bloecker H
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 652)
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                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKrZp434M1528"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
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   /note="Vector:
                   /lab_host="DH10B"
 pSport1; Site_1:
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NotI;
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                                                                                                                                                                                                                                       851
AGENCOURT_7907367 NIH_MGC_67
5', mRNA sequence.
BQ425358
                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                              EST
                                                                Contact: Robert Strausberg, Ph.D
                                                                               Unpublished (1999)
                                                                                             National Institutes of Health, Mammalian
                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 851)
                                                                                                                                                            Eukaryota;
                                                                                                                                                                             Homo sapiens
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                                                                                                      GTATTTATTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAA 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
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/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Lift
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Dest Local Similarity
                                1078 GGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAAT 1137
                                                                                                                                                            1018 GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 TTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGCATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                             GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACA 957
                                                                                              GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 439
                                                                                                                                                                                                                      TTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGAT
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AGENCOURT_6427660 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:55020755', mRNA sequence.
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Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
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                                                                                    AATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCA 661
  AATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCA 60
                                                                                                                              649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMM02 row: o column: 14
High quality sequence stop: 617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jnpublished (1999)
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                                                                                                                                                                                                                                      212
                                                                                                                              Conservative
                                                                                                                                                                                                                               /lab_host="DH10B (phage-resistant)",
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: Xhot; cuAn made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDWA synthesis kit
(Strategene) and Superscript II RT (Life Technologies)."
a 149 c 202 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE: 3530341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                             28.5%;
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                                                                                                                                             Score 613.2; DB 10
Pred. No. 1.4e-172;
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                                                                                                                                                                   Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                              Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                          TGAACATTACCCTCCGGAGGGTGCTGGTCGGAC-CCGAGCTGGTGTCATGGTGGTTGCT 658
                                                                                                                                                                                                                                                                                                                                        GCATGATGGTGACCTGGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGG-CTCCCCA 599
                                                                                                                                                                                                                                                                                                                                                               GCATGATGGTGACCT-GCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                   ANATGCTANACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAGGTG
                                                                                                                                                                                                                                                                                        ACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGAC 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTAC 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603040168F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180993
                                        BI822845
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/clone_lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
02 a 134 c 179 g 177 t
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Pred. No. 2.8
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ches 12; Indels 3;
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472 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                      488 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                  412 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG 471
                                                                                                                                                               428 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                   352 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                                                                         368 CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACCGAAACTCTCAGCAAGCTAT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TTCCAGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 247
                                                                                                                                                                                                                                                                                                                            292 CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                               232 GAAACAGTATGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 CCAGAGAAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11451 row: h column: 18
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Clone distribution: MGC clone distribution information can be
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/lab_host="DHIOB"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, site_2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_115"
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232 GAAACAGTATGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAA 291
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                                                                                        TTCCAGAATTCCTCAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 209
                                                                                                           TTTATGAATTCCTCAGAGAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA 171
                                                                                                                                                     606;
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                             CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1147)
11 (bases 1 to 1147)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BQ948186
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AGENCOURT_8878641 NIH_MGC_71
5', mRNA secure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 501.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                      /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_1: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
a 289 c 284 g 250 t
                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6464639"
                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_71"
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                                                                                                                                                  Score 586.6; DB 14
Pred. No. 1.7e-164;
0; Mismatches 14;
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                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 743)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                    /organism="Homo sapiens"
                                                                                                                                 Location/Qualifiers
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GAGAATGGTCAGGACAGATTCTCTGTGGAGAGGGCCTGGCAGAACGAAGAGAGGATGGGGACA 710
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                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
http://image.llnl.gov
plate: LLCM1808 row: o column: 16
High quality sequence stop: 703.
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Clone distribution: MGC clone distribution information can
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/db_xref="taxon:9606"
/clone="1MAGE:4906215"
/clone_1ib="NIH_MGC_17"
/tissue_type="Thabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; S:
Site_2: XhoI; cDNA made by oligo-dT pri
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602693716F1 NIH_MGC_97
    Eukaryota;
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BG722472.1 GI:14001659
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 8.7e-163;
                                                                                                     Homo sapiens cDNA clone IMAGE: 4825970
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                                                            534 TATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGCTGAACTTGT 593
                                                                                                                    521 CTTAAACCTATGTTGCAGAGAGATTTCATAACTTGCTCTGCCAGCTCGGGGATTGGATCA
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                                       TATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGT 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 752)

NHH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
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/clone_lib="NIH_MGC_97"
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CTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA - AAG
                                                            TAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGGCCAAAACAAAACTTGCCAATGGCA 304
                                                                                                              CACTTAGACAGACTTACAACAGCTGTGCCAGGCTTTGCATAAACCAAGAGACAGTATGTC 180
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Plate: LLAM8536 row: k column:
High quality sequence stop: 587.
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Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                Conservative
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/strain="CZECH II"
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                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11122 row: i column: 05
                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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BI103092
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                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 637)
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/db.xref="taxon:10090"
/db.xref="taxon:10090"
/clone="IMAGE:5044664"
/clone=lib="NCI:CGAPEKid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                       /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569;
           Unpublished (1999)
                                                                                                                                                                                                   DKFZp434D2317_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2317 3', mRNA sequence.
Contact: Bloecker H
                                                           Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 544)
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                             (Bloecker, et al.)
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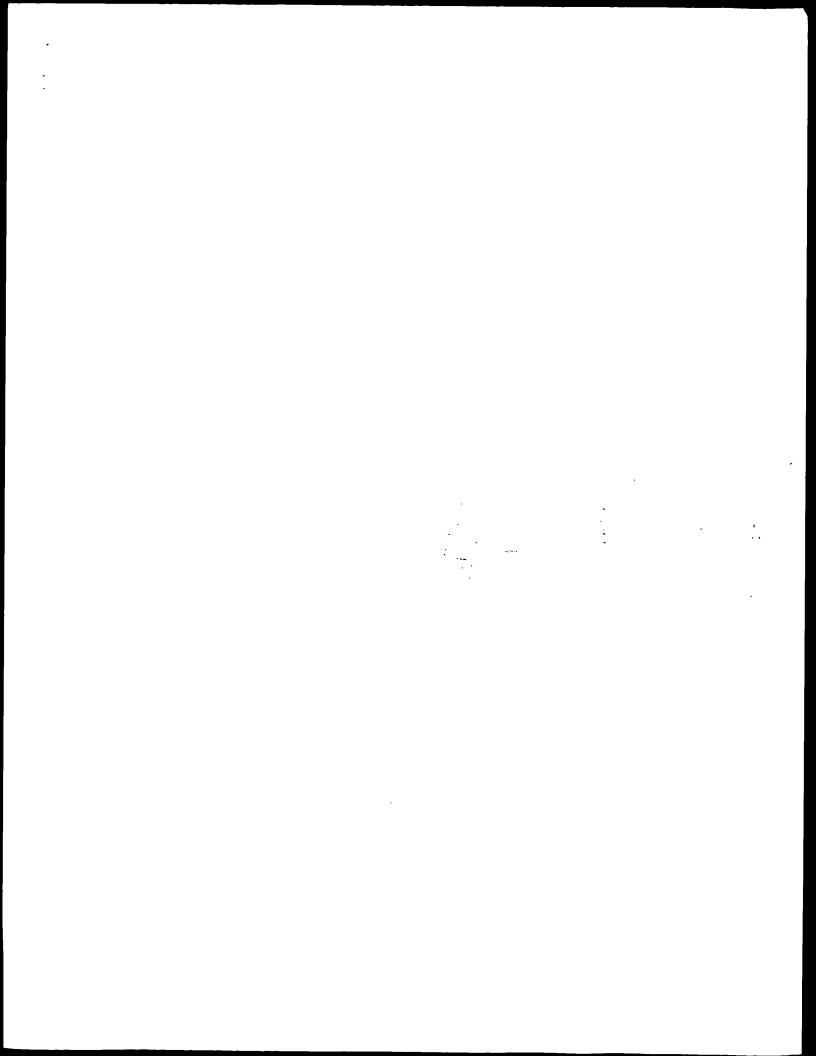
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BI455545 888 bp mRNA linear EST 21-AUG-2001 603173974F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253090 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKFZP434D2317) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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/note="Vector: pSport1; Site_1: NotI; Site_2:
, 102 c 153 g 138 t
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
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/db_xref="taxon:9606"
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Pred. No. 1.4e-147;
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                     CTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGACAAG 1272
                                                                                                                                                                                                    CGTTGATTCACCATTGTGAA-GCAGTTCTGCACTTGCGTTTCAATAATGGCATGATGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                        GCGGCCTTCGAGACAACACCATCAAGATCTGGGATAAAAGCACACTGGAATGCAAGCGGA 120
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    CTCAGGAGGGTGCTGGGGACACCGAGCTGCGGTCAATGTTGTAGACTTTGATGACAAG
                                                                                                                                                              CATTGATTCACCACTGTGAAGGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATGGTG
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                                                                                ACCTGTTCCAAAGACCGTTCCATCGCTGTGTGGGATATGGCTTCCCCCAACTGACATCACC
                                                                                                                      ACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BI455545
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High quality sequence stop: 684.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
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Clone distribution: MGC clone distribution information can
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5253090"
/clone_lib="NCI_CGAP_Mam5"
/tion:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: Not1; Cloned unidirectionally. Primer: Oligo d' Site_2: Not1; Cloned unidirectionally. Primer: Oligo d' Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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Pred. No. 4.8e-147;
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                                                                                                                                           CTGCTTTGGACCCGCGTGCTCCAAGCACGGGACTCTCATGTCTGCGGGACACTTGTTGCA
                                                                                                                                                          CTGCTTTGGACCCCCGTGCTGCAGGGACACTCTGTCTAC----GGACCCTTGTGGAG 1620
                                                                                                                                                                                                                    AACGGGATAGTGAGCGGAGCCTATGATGGGAACAATCAAACGTTGCTGCGCTCTTATGGC
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AGTTCCACTGATGACCACAATCTCATCTGGGACTTCCTGCATGATCCA 888
                                AGTTCACATGATGACACAATCCTCATCTGGGACTTCCTAAATGATCCA 1719
                                                                      CGCATTTCTGGCAAAAAGTTTTCCCGACCTCCAGTTTGGATGGCTTCCAGCATGGTCAGC
                                                                                                       C---ATTCCGGAAGAGTTTTTCGACTAC----AGTTTGATGAATTCCAG-ATTGTCAGT 167:
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Search completed: February 22, 2003, 00:36:50 Job time: 2816 secs



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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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sequence 19492, A
Sequence 2934, Ap
sequence 20, Appl
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	Seguence 473, App	Sequence 473, App	Sequence 473, App		•	Sequence 476, App	Sequence 14, Appl	Sequence 1, Appli	Sequence 5, Appli	Sequence 266, App	Sequence 119, App	Sequence 1590, Ap	Sequence 348, App	Sequence 124, App	N	Sequence 67, Appl	Sequence 218, App	Sequence 1690, Ap	Sequence 317, App	Sequence 101, App	Sequence 1196, Ap	Sequence 97, Appl				

ALIGNMENTS

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; LENGTH: 2151
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-042-417-1
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APPLICANT: Pagano, METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999
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Best Local
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CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
PRIOR FILING DATE: 2001-01-5
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181 AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTA
                                                                                                                61 TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAAT
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                                                                                                            ACTGACTGCTTCAGTGCTGCTATCAGAAGATGTCTTCTATCAATTGTGAATGATTGGAAC
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US-10-023-530-1
US-10-023-530-1
Sequence 1, Application US/10023530
Publication No. US20030007956A1
GEMERAL INFORMATION:
APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: HASSOT, ITina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH
FILE REFERENCE: B4717A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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US-09-764-848-15; Sequence 15, A
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Prior application data removed - NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                   GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ08
                                                                                                                                        Sequence 15, Application US/09764848 Patent No. US20020077270A1
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                                                        CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
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LOCATION: (1)..(657)
OTHER INFORMATION: Beta TrCP
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LOCATION:
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LOCATION: (941)
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NAME/KEY: SITE
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1018 GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA 107
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                                           TTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCTCCAGTATGAT
                                                                                                    GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACACA
                                                                                                                                                           TTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGAT
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                                                                                     GATGAAAAATTATCAGTGGCC-TCGAGATAATTCTATTAAGATATGGGATAAAAACCWGC
                                                                                                                                            TTGCAGAGGATTCAGTGCCGCTCTGAAAATAGTAAAGGTGTCTACTGTTTACAGTACGAT
                                                                                                                                                                                                                                                                                      TTCAAAAACCAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTATAGAGCACTTTAT
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                            CTGGAATGTTTGAAAGTGTTWACAGGACACACARGCTCTGK-CTCTGTCTGCAGTATGAT
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                                                                                                                                                                                                                                                                SEQ ID NO 2778
LENGTH: 479
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                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION: MAP TO APO00252.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 1.6
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                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                         PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: GB PRIOR FILING DATE: 2000-10-04
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PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/632,366
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                               PRIOR
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OTHER INFORMATION:
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APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                   APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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EXPRESSED IN ADULT LIVER, SIGNAL
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                                                                                                                                     GB 24263.6
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Pred. No. 3.3e-73;
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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FILING DATE: 2001-01-30
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                                                              TGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGG 1386
                                                                                                                                            GAGAAATACATCGTGTCTGCCTCTGGTGACAGGACCATCAAAGTCTGGAGCATGAGCACC 70
                                                                                                                                                                                 GACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACT 1326
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TGTGAATTTGCTCGTACTCTCAATGGGCACAAGCGAG---
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NN: EXPRESSED IN LUNG, SIGNAL = 2.6

NN: EXPRESSED IN HELA, SIGNAL = 3.1

NN: EXPRESSED IN BAT44, SIGNAL = 2.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.75

NN: EXPRESSED IN HEART, SIGNAL = 1.6

NN: EXPRESSED IN HEART, SIGNAL = 1.9

NN: EXPRESSED IN BRAIN, SIGNAL = 1.7

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

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74.3%;
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--TCTTGTCTCCAGTACAGG
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SEQ ID NO 2934
LENGTH: 319
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APPLICANT: Byatt, John C.
APPLICANT: Maythialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLE
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511,006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09213888A Patent No. US20020164683A1
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                                                                    SEQ ID NO 20
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                                                                                                                                                                               APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                                                                                          CURRENT APPLICATION NUMBER: US/09/213,8888 CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (261)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 13-LIB3058-049-Q1-K1-D1
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                       LENGTH: 1881
TYPE: DNA
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ORGANISM: Artificial Sequence
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Similarity 93.1%;
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: homo sapiens
US-09-213-888-20
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                                                                                     GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides
TITLE OF INVENTION: Encode Them
                                                                                                                                                                                                                                                              Sequence 20, Application US/09328877A Patent No. US20020177187A1
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Best Local
                      CURRENT APPLICATION NUMBER: US/09/328,877A CURRENT FILING DATE: 1999-06-09
NUMBER OF
                                                                      FILE REFERENCE: 6142
                                                                                                                                                                                                                                                                                                                                                                                                         1564 GTTAAAATCTGGGATAT 1580
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SEQ ID NOS: 27
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Pred. No. 2e-27;
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; Sequence 26, Application US/09213888A
Patent No. US20020164683A1
; GENERAL INFORMATION;
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polyper
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OTHER INFORMATION: Description of OTHER INFORMATION: homo sapiens
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Polypeptides and Polynucleotides

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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: homo sapiens US-09-213-888-26
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RESULT 10
US-09-328-877A-26
; Sequence 26, Application US/09328877A
; Patent No. US20020177187A1
; GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
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LENGTH: 2001
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US-09-213-888-24
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CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 2010
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APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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US-09-328-877A-24
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 24
LENCTH: 2010
TYPE: DNA
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APPLICANT: Gurney, Mark E.
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APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: V5HIS tagged OTHER INFORMATION: homo sapien
1447 ATCCGTGTTTGGGATGTGGAGACAGGGAATTGCATTCACACGTTAACAGGGCACCAGTCG 1506
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                                                  1423 ATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAA 1482
                                                                                                    1387 AGAGTCTATTCATTACAGTTTGATGGTATCCATGTGGTGAGTGGATCTCTTGATACATCA 1446
                                                                                                                                                                                                              1327 GTAAAGGTGTGGGATCCAGAGACTGAAACCTGTCTACACACGTTGCAGGGGCATACTAAT 1386
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                                                                                                                                                                                                                                                                                                                                                                       1243 GCTGTCAATGTTGTAGACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACT 1302
                                                                                                                                                            1267 GCAGTCCGCTGTGTTCAATATGATGGCAGGAGGGTTGTTAGTGGAGCATATGATTTTATG 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                            1216 TGGGATATTGAGACAGGCCAGTGTTT-----ACATGTTTTGATGGGTCATGTTGCA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1123 CACTTGCGTTTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTA 1182
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US-09-213-888-1
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APPLICANT: Gurney, Mapplicant: Li, Jinhe
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Best Local Similarity
Matches 340; Conserv
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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ORGANISM: Homo sapiens
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GTAAAGGTGTGGGATCCAGAGACTGAAACCTGTCTACACACGTTGCAGGGGCATACTAAT 1430
                                          ATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGA 1362
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                                                                                                                       GCTGTCAATGTTGTAGACTTTGATGACAAGTACATTGTTTCTGCCATCTGGGGATAGAACT 1302
                                                                                                                                                                                       TGGGATATTGAGACAGGCCAGTGTTT------ACATGTTTTGATGGGTCATGTTGCA 1310
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                                                                                              GCAGTCCGCTGTGTTCAATATGATGGCAGGAGGGTTGTTAGTGGAGCATATGATTTTATG
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Pred. No. 3.1e-27;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2485)
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; LOCATION: (3372)
US-09-328-877A-1
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LENGTH: 3550
TYPE: DNA
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Best Local Similarity
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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                                                                                                                            CACTTGCGTTTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTA 1182
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                                                                                                                                                                                                                                            TGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTG 1122
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                                             TGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCT 1242
                                                                                              TGTATGCATCTTCATGAAAAAAGAGTTGTTAGCGGTTCTCGAGATGCCACTCTTAGGGTT 1259
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US-09-213-888-2
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Best Local :
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LENGTH: 3571
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/213,888A CURRENT FILING DATE: 1998-12-17 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 6142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure LOCATION: (3393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (2506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
1161 TGGAATGCAGAGACTGGAGAATGTATACACACCTTATATGGGCCATACTTCCACTGTGCGT 1220
                                             1063 TGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTG 1122
                                                                                            1101 TCATCACAAATGAGAGACAACATCATTAGTGGATCTACAGATCGGACACTCAAAGTG
                                                                                                                        1003 TGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTG 1062
                                                                                                                                                                                         1041 TGGTCAGCAGTCACAGGCAAATGTCTGAGAACATTAGTGGGACATACAGGTGGAGTATGG 1100
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                                                                                                                                                                                                                                      943 TGGGATAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTC 1002
                                                                                                                                                                                                                                                                                   981 TGCTTACAGTTTTGTGGTAACCGAATAGTTAGTGGTTCTGATGACAACACTTTAAAAGTT 1040
                                                                                                                                                                                                                                                                                                                                883 TGTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATC 942
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                1543 ATTAAAGTGTGGGATCT 1559
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                                                                                                       TTAACAAGTGGAATGGAACTCAAAGACAATATTCTTGTCTCTGGGAATGCAGATTCTACA 1631
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Search completed: February 22, 2003, 02:00:32 Job time: 185 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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3034
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Gapop 10.0 , Gapext 0.5
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  Query
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-190-802A-30
US-08-477-346-30
US-08-477-3089-30
US-08-487-072A-30
US-08-190-802A-32
US-08-487-072A-32
US-08-487-072A-32
US-08-477-165A-29
US-08-190-802A-52
US-08-190-802A-51
US-08-190-802A-51
US-08-190-802A-51
US-08-190-802A-56
US-08-477-346-52
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Sequence 30, Appl
Sequence 2, Appli
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298.5	298.5	299.5	299.5	299.5	299.5	299.5	299.5	305	305	305	305	305	306	306	313.5	318	318	
9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.3	10.5	10.5	
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Sequence 18, Appl	Sequence 18, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 2, Appli	Sequence 26, Appl		Sequence 2, Appli	Sequence 62, Appl	Sequence 62, Appl	Sequence 62, Appl	Sequence 3, Appli	Sequence 62, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 52, Appl	Sequence 52, Appl	

ALIGNMENTS

US-08-190-802A-30 US-08-190-802A-30 Sequence 30, Applicat Patent No. 5519003 GENERAL INFORMATION: ETLING DATE: 01-FEB-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,87 TELEFAX: (415) 324-096 INFORMATION FOR SEQ ID NO: ZIP: 9430b-vov. ZIP: 9430b-vov. COMPUTER READABLE FORM: COMPUTER: Floppy disk COMPUTER: IBM PC compatible COMPUTER: CVSTEM: PC-DOS/MS-DOS TOPOLOGY: unknow... MOLECULE TYPE: peptide COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit TITLE OF INVENTION: WD-40 - De TITLE OF INVENTION: Thereof HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: REFERENCE/DOCKET NUMBER: 86 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880 NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: \ LENGTH: 517 amino acids STATE: C STREET: P.O. BOX APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-1994 INDIVIDUAL ISOLATE: TYPE: amino acid ADDRESSEE:), Application US/08190802A 5519003 CA P.O. Box 60850 (415) 324-0960 USA Dehlinger & WD-40 - Derived Peptides and BETA TRCP, Fig. 33,875 30: VON: VON: Associates Score 2582.5; DB 1; Pred. No. 2.9e-266; Uses

QΥ

18 SSEREDCHNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77

Query Match Best Local Sim: Matches 487;

Similarity

85.1%; 91.4%;

DB 1;

517; 31;

Indels Length

Gaps

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Conservative

DB 4;

Indels Length 517;

31;

Gaps

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RESULT 2
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       TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30
                                                       APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY_AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE_POCKET NUMBER: 2550-00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1005
CT.ACCTTOTAL
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Peni
CITY: Washington
STATE: DC
                                      TELEPHONE:
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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N: 514
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . TYPE: amino acid
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HYPOTHETICAL: N
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LENGTH: 517 amino acic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 TDITLRRVLVGHRAAVNVVDEDDKYIVSASGDRTIKVWNTSTCEEVRTLNGHKRGIACLQ 437
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                                                                        ZIP:
                                                                                       COUNTRY:
                                                                                                         STATE:
                                                                                                                      CITY: Washington
                                                                                                                                          STREET:
 OPERATING SYSTEM:
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91.4%;
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Pred. No. 2.9e-266;
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                                                                                                               RESULT 4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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                                                            Sequence 30, Patent No. 6
                                                GENERAL INFORMATION:
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NAME: MURASHIGE, KATE H.
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             APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 GTSSMIVPKORKLSANYEKEKELCVKYFEOWSECDQVEFVEHLISRMCHYOHGHINTYLK 102
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                                                                                                                                                                               VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMV 162
                                                                                                                                                                                                                                             YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
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                                                                                                                                                              VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 514
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                                                                 0, Application 6423684
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91.4%;
WD-40 - Derived Peptides and
                                                                                US/08487072A
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Pred. No. 2.9e
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Best Local S
Matches 487
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MOLECULE TYPE:
HYPOTHETICAL: 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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                  402 YRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                438 YRDRLYVSGSSDNTIRLWDIECGACLRYLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                342 TDITLRRYLVGHRAAVNVVDEDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                       378 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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Local Similarity 91.48;
es 487; Conservation
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                                                                                                                                                                                                                                 QRIHCRSETSKGYYCIQYDDQKIYSGLRDNTIKIWDKNTLECKRILTGHTGSYLCLQYDE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                  GTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
                                                                                                                                                                                                                 QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTGSVLCLQYDE
                                                                                                                                                                                                                                                                                 RTDSLWRGLAERRGWGQYLFKNKPPDGKTPPNSFYRALYPKIIQDIETIESNWRCGRHSL
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                                                                                                                                                                                                                                                                                                                                                   PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMV 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
                                                                                                                                                RVIITGSSDSTYRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
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Pred. No. 2.9e-266;
Pred. No. 2.9e-266;
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; ORGANISM: Saccharomyces cerevisiae
US-09-177-165A-30
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US-09-177-165A-30
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Best Local Similarity
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PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
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CURRENT FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/092,443
PRIOR FILING DATE: 1998-07-10
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
TITLE OF INVENTION: DEPENDENT PROTEOLYSIS
FILE REFERENCE: 11757.1005U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
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            583 -----KCMHTF---NGR--RLQRETQHTQTQSLGDKV 609
                                                           504 RAPAGTLCLRTLYEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                          526 LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                                                             466 VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 ---GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 --QELSIKIISYLDCQSICNATRVCRKWQKLADDDRVWYHMCEQHI-----DRKC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 GLDHIAENILSYLDAKSLCAAELYCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
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                                                                                                                                                 -----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP 503
                                                                                                                                                                                                                                                                                                          ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
                                                                                                                                                                                                                                                                                                                                                         ASPTDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH--- 429
                                                                                                                                                                                                                                                                                                                                                                                                          FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV 409
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 587 amino acids
TYPE: amino acid
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
                                         392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                           151 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG------VTIPDHIQP 203
                                                                                                                                                                                           263 QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 322
                                                                                                                                                                                                                                            274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                204 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                         176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 24-JUL:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1185 A CITY: New York STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                         WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD
                                                                                                WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA
                                                                                                                                                                                                                                                                                                                                            PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1185 Avenue of the Americas
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NO: 2:
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                                                                                                                                                                                                                                                                                             262
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Query Match 13.2%; Score 399; DB 1; Length 779; Best Local Similarity 24.3%; Pred. No. 3e-33; Matches 139; Conservative 80; Mismatches 196; Indels 156; Gaps 20; Qy 56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQW 108 1	COMPUTER REALABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATEONIN PC-LOSS/MS-DOS CURRENT APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-194 CLASSIFICATION NUMBER: US/08/190,802A ATTORNEY/AGENT INFORMATION: NAME: Fablan, Gary R. REGISTRATION NUMBER: 33,875 REFERENCE/DOCKET NUMBER: 33,875 REFERENCE/CHARACTION INFORMATION: TELEPHONE: (415) 324-0960 INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 779 amino acids TYPE: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15 US-08-190-802A-32	
FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H. REGISTRATION NUMBER: 2550-0025.20 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500 TELEFAX: (202) 887-1500 TELEFAX: (202) 887-0763 INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 779 amino acids TYPE: amino acids TYPE: mino acids TYPE: protein MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15 US-08-477-346-32	US-08-477-346-32 Sequence 32, Application US/08477346 Patent No. 6262023 GENERAL INFORMATION: APPLICANT: Mochly Rosen, Daria APPLICANT: Mochly Rosen, Daria APPLICANT: WID-40 - Derived Peptides and Uses TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESSE: MOTISON & FOETSET STREET: 2000 Pennsylvania Avenue, NW CITY: Washington STATE: DC COUNTRY: USA 21P: 20006-1812 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER SYSTEM: PC-DOS/MS-DOS SOFTWARE: DATE: DC OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CUASSIFICATION NUMBER: US/08/477,346 FILING DATE: 07-JUN-995 CLASSIFICATION NUMBER: 08/487,072 APPLICATION NUMBER: 08/487,072	Oy 277 DQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVMDVN 335

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US-08-473-089-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
TUMBER OF SEQUENCES: 265
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APPLICANT:
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                                        APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG 528
                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Peni
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 TINSLGVSQNWNKTIRKSTSLWKKLLISENFV---------SPKGF 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 -----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED 294
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                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Morrison & Foerster STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
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                                                                  07-JUN-1995
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                                                                                          US/08/473,089
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                                                                                                                                                                                                                   RESULT 10
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                                                                                                                     Sequence 32, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Dei
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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24.3%; Pred. No. 3e-33;
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LENGTH: 779 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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NAME: MURASHIGE, KATE H.
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             487 AYDGKIKVWDL----
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TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 29,959
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CLASSIFICATION:
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                                                                                                                         LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
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                                                    HMASYRTVSGHGNIVVSGSYDNTLIVMDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA
                                                                       HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG
                                                                                                                                                           VDFDD----KYIVSASGDRTIKVWNT-----
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2000 Pennsylvania Avenue,
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24.3%; Pred. No. 3e-33;
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---VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS
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SEQ ID NO 29
LENGTH: 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN TITLE OF INVENTION: DEPENDENT PROTECLYSIS FILE REFERENCE: 11757.10USU1
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APPLICANT: Willems, Andrew
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536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566 : | :| || || || || || ::|
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                                                                                                                                                                                                                                                                  SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                          AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                                                                                                                                                                          HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
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                                                                                                                                                     HMASVRTVSGHGNIVVSGSYDNTLIVWDVAQMKCLYILSGHTDRIYSTIYDHERKRCISA
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE TITLE OF INVENTION: AND METHODS OF USE THEREFOR
        496
                                    249 NWRCGRHSLQRIHCRSETSKG----VYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILT 304
                                                                                  474
                                                                                                                      189
                                                                                                                                                            453 ----
                                                                                                                                                                                      129 HGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGML 188
                                                                                                                                                                                                                              405 SRQLFVSNDGNTLNTNKERSKSKSIDLEKPEILIN--NKKKESINLETIK------ 452
                                                                                                                                                                                                                                                                                                      345 LIFPDTSERDNNNNNNNNNNNNNNNNNNNNNNNNNNNNSSISKSLVEISSGSKERNDRDSP 404
                                                                                                                                                                                                                                                                73 TK---LANGTSSMIVPKORKLSASYEKEK-ELCVKYFEOWSESDQVEFVEHLISOMCHYO 128
                                                                                                                                                                                                                                                                                                                                            13 LKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                  FTGCSDNSIRV----
                                                                                                              WKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIES 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                              12.9%; Score 392; DB 4; Length 732;
24.1%; Pred. No. 1.5e-32;
ative 84; Mismatches 172; Indels 118; Gaps
-QTLKGHEGPVESICYNDQYLFSGSSDHSIKVWDLKKLRCIFTLE 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
                                                                                                                                                    -----LIETIKGYHVTSHLC----IC-----DNLL 473
                                                                              ·--YDYKS---
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                                                                          ---- QNMECV-- 495
                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                          US-08-283-917-3
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                  Matches
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                                                                                                                                                                                                                          LENGTH:
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              87;
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Sequence 3, Applic Patent No. 5849557
                       Query Match 11.7%; Score 354; DB 2; Length 409; Best Local Similarity 29.2%; Pred. No. 6.4e-29;
                                                                                                                                                                                                                                                                      TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/ACENT INFORMATION:
NAME: Oblon, No. 5849557man F.
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: OXIDIZED PHOPHOL TITLE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: INOUE, KEIZO APPLICANT: ARAI, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 NDKTIKVWDLKT---FRCNYTLKGHTKWVTTICILGTNLYSGSYDKTIRVWNLKSLECSA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 KDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 GHDKPVHTVLLNDKYLFSGSSDKTIKVWDLKTLECKYTLESHARAVKTLCISGQYLFSGS 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 GHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRENNGMAVTCS 364
                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Oblon, No. 5849557man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/283,917 FILING DATE: 03-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C.
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                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                              409 amino acids
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    Conservative
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                                                                                                                 Bos taurus
                                                                                                                                                                                  unknown
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      peptide
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                                                                                                                                                                                                       unknown
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    57; Mismatches 110;
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  Indels
  44;
Gaps
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MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Bos
US-08-961-716-3
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                                                                                                                                                                    TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: 1/2
CITY: Arlington
STATE: Virginia
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ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER &
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 KTLRVWDY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 VRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 ETKKSGKPGPFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHSGGKFILSCADD 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/961,716 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                      TOPOLOGY:
                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKMWEVQTGYCV---KTFTGHREWVRM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMLNTLIHHCEAVLHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------LVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSGAYD 489
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                                                                                                                          amino acids
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                                                                                                                                                                                                                                     (703) 413-2220
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SYSTEM: PC-DOS/MS-DOS
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; MOLECULE TYPE: US-08-283-917-9
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GENERAL INFORMATION:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: AND GENE THEREOF
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                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 03-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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amino acid
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INOUE, KEIZO
ARAI, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1994
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                                                               338 EMINTLIHHCEAVLHLRF--NNGMMYTCSKDRSJAVWDMASPTDITLRRVLVGHRAAVNV 395
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Result
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Maximum Match 100%
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1: sp_archea:*
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-99075339; PubMed=9859996;
Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A. Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;

"Identification of the receptor component of the IkappaBalpha-ubiquitin ligase,";
Nature 396:590-594(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QUI5 PRELIMINARY; PRT; 569 AA.
Q9QUI5;
Q1MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Ubiquitin ligase FWD1 (Beta-transducin repeat containing
(F-DOX-WH40 repeat protein 1).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE FROM N.A.
STRAIN=129/SV;
MEDLINE=21601157; PubMed=11735228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-99199275; PubMed-10097128;
Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumot Hatakeyama S., Kitagawa M., Nakayama K., Onoe K., Good Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good Nakayama K.
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Q969н0

Q969h0

homo sapien musculu

Q8VHP4 Q8VBV4

Q96A16 Q96LE0

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98.8 98.5 798.3 778.3 78.9 668.9 40.5 40.5 40.5 21.1 21.1 21.1 21.1 21.1 21.1

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Q9BJ54 L Q922C7 Q9VZF4 Q9NUX6 Q96RI2

Q922c7 mus musculu Q9vzf4 drosophila Q9vzf4 drosophila Q9nux6 homo sapien Q96ri2 homo sapien Q96le0 homo sapien Q96al6 homo sapien

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044382

Score 2997 2990 2978

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Description

Q9QUI5 Q9Z159

Ogqui5 mus musculu Ogz159 mus musculu Ogr1g7 mus musculu Og23h0 mus musculu

044382 drosophila Q9vde3 drosophila Q9bj54 heterodera

drosophila drosophila

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EMBL; AF391189; AAL40929.1; J
MGD; MGI:1338871; Btro.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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SEQUENCE
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SMART; SM0320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50234; WD_REPEATS_REGION; 1.
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Genomics 78:214-222(2001)
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Nakayama K.-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of a Mouse Gene (Fbxw6) That Encodes a Homologue Caenorhabditis elegans SEL-10.";
                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC 420
                                                                                                                                                        RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNAGEMLNTLIHHCEAVLHLRENNGMM
                                                                                                                                                                          RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
                                                                                                                                                                                                                                                       QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                                                                                                 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF391182; AAL40929;
AF391183; AAL40929;
AF391184; AAL40929;
AF391185; AAL40929;
AF391186; AAL40929;
AF391187; AAL40929;
AF391187; AAL40929;
    EFVR"ILNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIREDN
                                                                            VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
                                                                                                                                                                                                                                   QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECK
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AF391178;
AF391179;
AF391180;
AF391181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; WD repeat.
E 569 AA; 65105 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; AAL40929.1; JOINED.
3; AAL40929.1; JOINED.
3; AAL40929.1; JOINED.
4; AAL40929.1; JOINED.
4; AAL40929.1; JOINED.
5; AAL40929.1; JOINED.
6; AAL40929.1; JOINED.
7; AAL40929.1; JOINED.
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3; Mismatches
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Pred. No. 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 560;
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Pfam; PF00400; WD40; 7
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Q9Z159;
Q1-MAY-1999 (TrEMBLrel.
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  301
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PRINTS; PRO0320; GPROTEINBRPT.
PRODOM; PRO030018; WDA0; 4.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50084; WD_REPEATS_REGION; 1.
Repeat; WD repeat.
SEQUENCE 569 AA; 65047 MW; BC7C7A44815BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Signal-induced ubiquitination of IkappaBalpha Slimb/beta-TrCP;" Genes Dev. 13:284-294(1999).
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP | EMBL, AF112979; AAD04181.1; -. MGD; MGI:1338871; Btrc. InterPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99145465; PubMed=9990853; Spencer E., Jiang J., Chen Z.J.;
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InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-transducin repeat containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 ILIWDFLNDPAAHAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                            1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRENNGMM
                                          QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECK
                                                                     QDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                          ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                                     ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                                                                 STAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
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                                                                                                                                                                       RVTSDGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
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569 AA; 65047 MW; BC7C7A44815BED96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.5%; Score 2990; 98.4%; Pred. No. 2.
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Last annotation update)
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SMART; SM00320; WD40; 7.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS500878; WD_REPEATS_1; UNKNOWN_6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50234; WD_REPEATS_REGION; 1.

Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Beta-transducin repeat-containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9R1G7;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winston J., Elledge S.J., Harper J.W.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R1G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00320; GPROTEINBRPT PRODOM; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF110396; AAD41025.1;
MGD; MGI:1338871; Btrc.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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                                                                                                                                                                                                                                                                              MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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                                                                                                                                                                      STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                                                                                                                                                                                    {\tt MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLT}
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RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                  STAMKTENCVAKAKLANGTSSMTVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                  ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHITENILSYLDAKSLCAAELVCKEWY
                                                                                      ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             65209 MW;
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97.9%;
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                                                                                                                                                                                                                                                                                                                      Score 2978; DB 11;
Pred. No. 3.2e-251;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                             E6DDCAD28D551D9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                Length 569;
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                                                                                                                    Query Match
Best Local S
Matches 440
                                                                                                                                                                                                                                                                                      0923H0 PRELIMINARY; PRT; 563 AA. 0923H0; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBXW1B
                                                                                                                                                                                                                             Prodom; PD000018; WD40; 4.
PROSITE; PS5006181; FBST, WD_REPEATS_1; UNKNOWN_5
PROSITE; PS50082; WD_REPEATS_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F-box/WD40 repeat-containing
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                Repeat; WD
                                                                                                                                                                                                              PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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45 VRCLQNTSVMEDQNEDESPKKSALWQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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                            TVCLASTA-MKTEN-----CVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQW 108
                                                           MEP-DSVIEDKTIELMCSVPRSLWLGCAN---
                                                                                        MDPAEAVLQEKALKEMNSSERE----DCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQ--E
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                                                                                                                                   Similarity
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                                                                                                                                                                                                repeat
                                                                                                                        Conservative
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                                                                                                                                                                                64741 MW;
                                                                                                                                    75.3%;
75.7%;
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                                                                                                                    Score 2286; D
Pred. No. 8e-1
46; Mismatches
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                                                                                                                                                                                   9AB562F3FF5E3496 CRC64;
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                                                                                                                    36; DB 11;
. 8e-191;
cches 65;
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n skin tumor
                                                           -LVESMCALSCLQSMPS
                                                                                                                        Indels
                                                                                                                                                   Length 563;
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                                                                                                                      Gaps
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     Query Match
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01-JUN-1998
01-JUN-1998
                                                                                                  PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang J., Struhl G.;
"Regulation of the Hedgehog and Wingless signalling pathways
box/MD40-repeat protein Slimb.";
Nature 391:493-496(1998).
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AF032878; AAC38521; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIMB (
                                                           SEQUENCE
                                                                                                                                                                                                                                             PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                               Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0023423; slmb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98121115;    PubMed=9461217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFQIISSSHDDTILIWDFLNVPPSAQNETRSPFRTYTYISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLOFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEG
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                                                                                                                                                                                                                                                                                                     PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKIWDKSSLECLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDDKIISGLRDNS
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                                                                                                                                                                                  SM00256; FBOX;
SM00320; WD40;
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(TrEMBLrel. 06,
(TrEMBLrel. 20,
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                                                        58952 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
  Score 2089.5;
                                                     DBB0243D3730A5E8 CRC64;
DB
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5,
                                                                                                                                                                                                Length 510
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Q9VDE3

ID Q0

ACD Q0

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                                                                                                                                                                                                                                                                  MEDIINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                      Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botthan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLMB protein (SLIMB).
SLMB OR CG3412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VDE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 MKTENCVAKTKLANG---TSSMIVPKORKLSAS--YEKEKELCVKYFEOWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 HLLSRMCHYQHGQINAYLKPMLQRDFITLLPIKGLDHIGENILSYLDAESLKSSELVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 METDKIMDETN-SNAQAFTTTMLYDDVRKKDSSPTYQTERELCFQYFTQWSESGQYDFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTILIWDFLNFTPNENKTGRTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTILIWDFLNDPAAQAEPPRSPS 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNSIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMNDIDSIENNWRTGRHMLRRINCRSENSKGVYCLQYDDGKIVSGLRDNTIKIWDRTDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQVDDQKIVSGLRDNTIKIWDKNTLE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WLRVISEGMLWKKLIERKVRTDSLWRGLAERRNWMQYLFKPRPGQ-TQRPHSFHRELFPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394;
       K., Doup L.E., Downes M.,
K.J., Evangelista C.C., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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       Ferriera
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Virskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.";
Exception of the sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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"Drosophila null slimb clones transiently deregulate Hedgehog-
independent transcription of wingless in all limb discs, and induce
decapentaplegic transcription linked to imaginal disc regeneration.";
Mech. Dev. 93:15;26(2000).

1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).

EMBL; AE00373; AAF558531; -
EMBL; AF222924; AAF63213.1; -
EMBL; AF222924; AAF63213.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0023423; slmb.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=OVARY, AND IMAGINAL DISC; MEDLINE=20245299; PubMed=10781936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris
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      299
                                            182
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                                                                                                                                                                                                                                                                                                                        MKTENCVAKTKLANG---TSSMIVPKQRKLSAS--YEKEKELCVKYFEQWSESDQVEFVE 118
    CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                         WLRVISEGMLWKKLIERKVRTDSLWRGLAERRNWMQYLFKPRPGQ-TQRPHSFHRELFPK 181
                                                                                                                                            METDKIMDETN-SNAQAFTTTMLYDPVRKKDSSPTYQTERELCFQYFTQWSESGQVDFVE
                                                                   IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                                                                                                                       HLLSRMCHYQHGQINAYLKPMLQRDFITLLPIKGLDHIAENILSYLDAESLKSSELVCKE
                                                                                                                                                                                                                                            HLISOMCHYOHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00646; F-box; PF00400; WD40;
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a D., H
                                            IMNDIDS I ENNWRTGRHMLRR I NCRS ENSKGVYCLQYDDGK I VSGLRDNT I K I WDRTDLQ
                                                                                                                                                                                                                                                                                                                                                                      394;
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A., Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00256; FBOX; 1.
SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 AA; 58952 MW;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                       68.9%;
78.3%;
                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                       Score 2089.5; D
Pred. No. 9.8e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 F4D5DF126F58A012 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                              510;
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Best Local
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Heterodera glycines (Soybean Cyst nematode).
Eukaryota, Metazoa, Nematoda, Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BJ54;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00320; GPROTEINBRPT.
Prodom; PD000018; WD40; 4.
SMART; SM00320; WD40; 7.
SPROSITE; PS00678; WD_REPEATS_1; UNKNOWN_6.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ-i-SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASE EMBL; AF339101; AAK26376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ВJ54
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
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"Plant parasitic nematode b-TRCP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=51029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
 417
                               181
                                                            357
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                                                                                                                                                                                                                                              193 IERMVRTDSLWRGLAERRGWGQYLFKNK-------PPDGNAP---PNSFYRALY 236
                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN
                                                                                                                                                                       PKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTILIWDFLNFTPNENKTGRTPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
TSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCI
                               DGMLVTCSKDRSIAVWDMASPRDIEVRRVLVGHRAAVNVVDFDHKYIVSASGDRTIKVWN
                                                                                          LGCVQTLSGHTGSVLCLQYDNQMIASGSSDATVRIWDVNTGEQLKTLVHHCEAVLHLRFQ 180
                                                                                                                       LECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFN 356
                                                                                                                                                     PKITADIRQIEQNWREGRHRLERINCQSENSKGVYCLQYDDEKIISGLRDNTIKIWSRPS 120
                                                                                                                                                                                                                IERQVRNDALWAGLAIRRGWKKYFFCSKDQATRAISQSWRQPKNGEDALEFQHKFYRELY 60
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                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                         430 AA;
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                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                             Score 1498; DB 5;
Pred. No. 3.2e-122
                                                                                                                                                                                                                                                                                                                                         4ABC3FF2DFE3A50B CRC64;
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RESULT
Q9VZF4
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AC Q9
DT 01
DT 01
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Best Local
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      Q9VZF4;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                   Q9VZF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00320; GPROTEINBRPT.
PRODOM: PD000018; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001680; wD40. Pfam; PF00400; wD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:2144023; Fbxw1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FBXW1B
                                                                                                                                                                                                                                                     181
                                                                                                                                                                       241 RSPSRTYTYISR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASP 377
                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 5 WD.; BC008552; AAH08552.1;
                                                                                                                                                                                                                                               VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPP 557
                                                                                                                                                                                                                                                                                                                                                YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                                                                                                                                                 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                             RSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                               YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                                                                       TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFDSKRIVSGAYDGKIMIWDLAAALDPWTPPNSICIKTLSQHTGRVFRLQFDEFQIISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASTCEFVRTLNGHKRGIACLQYRDRLIVSGSSDYSIRLWDIECGNCLRVLEGHEELVRCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDDTILIWDFLNTGPSAAVAAGAAAAAHNQAVQHHQAAPAAQPA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
      (TrEMBLrel. 13, (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 AA;
                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%; Score 1230; 92.9%; Pred. No. 3
      Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F71737CBD7A9F75F CRC64;
                                                                   1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536
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    Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Walson C.R., Millos G.L.G., RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Podeson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wein M.-H., Liegwam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Reinert K., Remington K., Sampeon M., Skupski M.P., Smith T., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Welson D.A., Weinstock G.M., Weissenbach J., RA Wirskas R., Tector C., Furner R., Venter E., Wang A.H., Wang X., Pan S., Wang S., Wao Q., Zheng L., Wang S., Wao Q., Zheng L., Wang S., Wao Q., Zheng L., Wang S., Wao Q., Zheng J., Wang S., Wao Q., Zheng L., Wang S., Wao Q., Zheng L., Wang S., Zhon M., Zhong G., Zhao Q., Zheng L., Wang S., Zhon M.,
                                                                                                           Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George Gonzalez M., Guarin H., Li P., Liao G., Minanda A., Mungall C. Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wa Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
                                                                                Submitted (JAN-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                   -1- SIMILARITY: CONTAINS 7 WD REPEATS EMBL; AE003480; AAG22246.1; -.
                                                                                                   Celniker S.;
                                                                                                                                                                                                                     STRAIN-BERKELEY;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGO OR CG15010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last annotation update) CG15010 protein (LD21322p) (LD30271p).
AAL28848.1;
AAL68231.1;
                                                       EMBL/GenBank/DDBJ databases.
WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                     Park S.,
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Q9NUX6
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Best Local
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Pfam; PFOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00256; FBOX; 1.
SMART; SM00326; WD40; 1.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50282; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00646; F-box; 1 Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0041171; ago.
InterPro; IPR001810; F-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                 ONUXA;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004
                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 protein
                                                                                                                                                                                                                CDNA FLJ11071 fis, clone
                                                                                                                                                                                                                                                                                                         Q9NUX6
                                                                                                                                                                                                                                                                                                                                                                                                 1232 SGPNKHHSAVTCLQFNSRFVVTSSDDGTVKLWD 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   852 FORWSHVERLLALDRLIDHCDPSQVRHMMKVIEPQFQRDFISLLPR----ELALFVLSYL 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 FEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYL 164
                                                                     TISSUE-PLACENTA;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 DAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPP-- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNRIVSGSDDNTLKVWSAVNGKCLRTLVGHTGGVWSSQMSGNIIISGSTDRTLKVWDMD 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPKDLLRAAQTCRSWRFLCDDNLLWKEKCRKA-----QILAEPR-----SDRPKRG 953
                                                                                                                                                                                                                                                                                                                                                                                                                               V---EHSGRVFRLQFDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDGNMPPIASPWKAAYMR--QHI--IEMNWR-----SRPVRKPKVLKGHDDHVITCLQF 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DGNAPP-NSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKG-----VYCLQY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVETGNCKHTLMGHQSLTSGMELRQNILVSGNADSTVKVWDITTG-----QCLQTL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIECGACLRVLEGHEELVRCIREDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTL 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQYDGKLIVSGAYDYMVKIWHPERQECLHTLQGHTNRVYSLQFDGLHVVSGSLDTSIRVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLW 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGACVHTLQGHTSTVRCMHLHGSKVVSGSRDATLRVWDIEQGSCL---HVLVGHLAAVRC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1326 AA; 141360 MW; 3F42C873CFA3027F CRC64;
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                  PLACE1004937, moderately similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76;
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                                                                                                                                                                                                                                                                                                            553
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                    J., Wakamatsu
                                                        Suzuki Y.,
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 S DT DT AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL; AK001933; BAA91986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5

PROSITE; PS50082; WD_REPEATS_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; pF00646; F-box; 1.
pfam; pF00400; wA40; 7.
prints; pr00320; GPROTEINBRPT
proDom; pD000018; wD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50294; WD_REPEATS_REGION; 1.
                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation updat
F-box protein FBX30 (Fragment).
Homo sapiens (Human).
                                                                                             Q96RI2;
                                                                                                               Q96RI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                           495
                                                                                                                                                                                                                                                                                 444 NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                           ₹
                                                                                                                                                                                                                                                                                                                  AYDGKIKVWDLVAALDPRAPAGTLCLRTLV----EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESNWRCGRHSLORIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167;
                                                                                                                                                                                                                                                                                                                                                       QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                                                                                                                                            NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                                                                                                                                                                                                                                                                               ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                           496
                                                                                                                                                                                                                                              545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.1%; 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 640; DB 4;
Pred. No. 3.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA829C221986A3F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 211;
                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 553;
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Pfam; PF00646; F-box; 1.

Pfam; PF00400; WD40; 7.

ProDom; PD000018; WD40; 2.

PROSITE; PS50181; FB0X; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koepp D.M., Winston J.T., Harper J.W., Elledge S.J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
'- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
EMBL, AF383178; AAK60269.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20003061; PubMed=10531037; Winston J.T., Koepp D.M., Zhu C., Elledge "A family of manmalian F-box proteins."; Curr. Biol. 9:1180-1182(1999).
                                                                                                                  544 WD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 ESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIYSGLRDNTIKIWDKNTLECKRILTGH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 KLANGTSSMIVPKORKLSASYEKEKEL -- CVKYFEQWSESDQVEFVEHLISQMCHYOHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                      AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                             NADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                                                                                                                                                                                                                   QGHTNRYYSLQFDGTHYVSGSLDTSTRYWDYETGNCTHTLTGHQSLTSGMELKDNTLYSG
                                                                                                                                                                                                                                                                         NGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
                                                                                                                                                                                                                                                                                                                    ATLRYWDIETGOCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                            RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL
                                                                                                                                                                                                                                                                                                                                                                                                       TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL----VPCSA----TPTTFGDL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167;
                                                                          504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63165 MW; B81CC1E2206B0D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 640; DB 4; 30.8%; Pred. No. 3.7e-47; tive 92; Mismatches 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.J., Harper J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72;
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                                                                                                                                                                                                                                                                                                                      391
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Interpro; IPRO01680; WD40.
Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
Probom; PD000018; WD40; 2.
PROSITE; PS50181; FB0X; 1.
PROSITE; PS50082; WD_REPEATS_1; UNKNOWN_5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50082; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat.
SEQUENCE 589 AA; 66120 MW; 2AFB6E8A36E6E8DE CRC64;
480 NADSTVKIWDIKTG-----QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL
                                        487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI
                                                                                                                                                                                      363
                                                                                                                                                                                                               367 RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS) EMBL; AY008274; AAG16640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R., Buhl A.E., Gurney M.E.;
"SEL-10 Interacts with Presentlin 1, Facilitates Its Ubiquitination, and Alters A-beta Production.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                            303 TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                  307 TGSVLCLOYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                                                                                                                                                                                                                                                                                             244 DTNWRRGELKSPKV-LKGHDDHVTTCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                  206 KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                     247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F-box protein SEL10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 KLANGTSSMIVPKORKLSASYEKEKEL--CVKYFEOWSESDOVEFVEHLISOMCHYOHGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 KLDHGSEVRSFSLGKKPCKV----SEYTSTTGL-----VPCSA-----TPTTFGDL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCAL
                                                                                   QGHTNRYYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                              NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                        ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                        ESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 640; DB 4
30.8%; Pred. No. 4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB_4; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72;
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15;

Matches Query Match

SEQUENCE

NON_TER Repeat;

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EMBL; AF411972; AAL06291.1; -.

REMBL; AY03353; AAK57547.1; -.

InterPro; IPR001810; F-box.

InterPro; IPR001810; F-box.

InterPro; IPR001680; WD40.

Pfam; PF00400; MD40; 7.

Pfam; PF00400; MD40; 7.

PFAm; PF00400; MD40; 7.

PFOSITE; PS0078; WD-REPEATS_1; UNKNOWN_5.

PROSITE; PS0078; WD_REPEATS_2; 7.

PROSITE; PS50082; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-21449047; PubMed-11565033;
MEDLINE-21449047; PubMed-11565033;
Moberg K.H., Bell D.W., Wahrer D.C., Haber D.A., Hariharan I.K.;
"Archipelago regulates Cyclin E levels in Drosophila and is mutated human cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Archipelago beta form (F-box protein FBW7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winston J.T., Koepp D.M., Zhu C., Elledge S.J., "A family of mammalian F-box proteins."; Curr. Biol. 9:1180-1182(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koepp D.M., Winston J.T. submitted (APR-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20003061; PubMed=10531037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Local Similarity
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                                                                                                                                                                                                    KLANGTSSMIVPKQRKLSASYEKEKEL - - CVKYFEQWSESDQVEFVEHLISQMCHYQHGH
DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                        KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                   LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                          INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK
                                                                                                                                                                         RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                 KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL
                           ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                             167;
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E 627 AA; 70324 MW;
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                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                       21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Harper W., Elledge S.J.; the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                        Score 640; DB 4;
Pred. No. 4.4e-47;
)2; Mismatches 211
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                                                                                                                                                                                                                                                                                                                     Length 627;
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REMBL; AY049984; AAL07271.1; -.

REMBL; AF411971; AAL06290.1; -.

RINTERPO; IPR001810; F-box.

InterPro; IPR001880; WD40.

RPfam; PF00406; F-box; 1.

RPfam; PF00406; F-box; 1.

RPfam; PF00400; WD40; 7.

RPFAM; PF00400; WD40; 2.

RPROSITE; PS05078; WD_REPEATS_1; UNKNOWN_5.

RPROSITE; PS05078; WD_REPEATS_2; 7.

RPROSITE; PS50082; WD_REPEATS_REGION; 1.
                                                                                               Matches 167;
                                                                                                                                              Query Match
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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MEDLINE=21449048; PubMed=11565034;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
F-box protein CDC4 (Archipelago alpha form).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21449047; PubMed=11565033; Moberg K.H., Bell D.W., Wahrer D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutated in a breast cance Nature 413:316-322(2001).
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                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:311-316(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Archipelago regulates Cyclin E human cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Human F-box protein hCdc4 targets cyclin mutated in a breast cancer cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed S.I
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                                           14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
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  KLDHGSEVRSFSLGKKPCKV----
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                                                                                                                       21.1%; 30.8%;
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Last annotation update)
                                                                                                                       Score 640; DB 4;
Pred. No. 5.2e-47;
                                                                                                                                                                                            E4A357F76DFD8203 CRC64;
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                                                                                               Mismatches
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  -SEYTSTTGL----
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                                                                                                                                         Length 707;
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RESULT 15
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                                      Query Match
Best Local :
         Matches 167;
                                                                                               PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

SEQUENCE 629 AA; 70562 MW; BE916405A3490A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VHP4;
                                                                                                                                                                                                                                                                          SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; aF427101; AAL50052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBWD6
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00646; F-box; 1
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-box protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ilyin G.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADSTVKIWDIKTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCKE-----EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
21.1%; Score 639; DB 11; Length 629; 30.8%; Pred. No. 5.4e-47; tive 92; Mismatches 211; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---QCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKL 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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   72;
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   Gaps
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                                     544 WD 545
                                                                        520 NADSTVKIWDIKTG------QCLQTLEGPSKHQSAVTCLQFNKNFVITSSDDGTVKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 INSYLKPMIQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                                                             284 DINWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 KLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                                    QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
                                                                                                                                                                        NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG
                                                                                                                                                                                                                                                                                                                                                   TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                            AYDGKIKVWDLVAALDPRAPAGTLCLRTL---VEHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                                                                                                                                                                                                 ATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                                                                                                                                                                                                                                                                      RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLDHGSEVRSFSLGKKPCKV-----SDYTSTTGL-----VPCSA-----TPTTFGDL 134
                                                                                                                                                                                                                                                                                                              TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRD 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 189
                                                                                                                                                                                         486
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Search completed: February 20, 2003, 09:55:19 Job time: 44 secs

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OM protein - protein search, using sw model
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                                                                                                                                                                                        Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/U;

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3: /cgn2_6/ptodata/1/pubpaa/U;

4: /cgn2_6/ptodata/1/pubpaa/U;

5: /cgn2_6/ptodata/1/pubpaa/U;

6: /cgn2_6/ptodata/1/pubpaa/U;

7: /cgn2_6/ptodata/1/pubpaa/U;

8: /cgn2_6/ptodata/1/pubpaa/U;

8: /cgn2_6/ptodata/1/pubpaa/U;

8: /cgn2_6/ptodata/1/pubpaa/U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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1038.379 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length		DB	ID	Description
_ :	3034	100.0	569	12	US-10-042-417-2	Sequence 2, Appli
N	1163	38.3	219	9	US-10-023-530-2	Sequence 2, Appli
ω	989.5	32.6	265	10	US-09-764-848-30	Sequence 30, Appl
4	644.5	21.2	626	9	US-09-213-888-21	Sequence 21, Appl
υī	644.5	21.2	626	9	US-09-328-877A-21	Sequence 21, Appl
თ	640	21.1	540	9	US-09-213-888-7	Sequence 7, Appli
7	640	21.1	540	9	US-09-213-888-10	Sequence 10, Appl
æ	640	21.1	540	φ	US-09-328-877A-7	Sequence 7, Appli
9	640	21.1	540	9	US-09-328-877A-10	Sequence 10, Appl
10	640	21.1	545	9	US-09-213-888-6	Sequence 6, Appli
11	640	21.1	545	9	US-09-328-877A-6	0
12	640	21.1	553	9	US-09-213-888-5	Sequence 5, Appli
13	640	21.1	553	9	US-09-328-877A-5	Sequence 5, Appli
14	640	21.1	559	9	US-09-213-888-9	Sequence 9, Appli
15	640	21.1	559	9	US-09-328-877A-9	Sequence 9, Appli
16	640	21.1	589	9	US-09-213-888-8	Sequence 8, Appli
17	640	21.1	589	9	US-09-328-877A-8	Sequence 8, Appli
18	640	21.1	592	9	US-09-213-888-4	Sequence 4, Appli
19	640	21.1	592	9	US-09-328-877A-4	Sequence 4, Appli

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246.5) E	260.5	264.5	283	293.5	296.5	299.5	299.5	307.5	316.5	334.5	337	337	384	392	399	455.5	545	575	640	640	640	640	640	640
8.1	0 0	8 6	8.7	9.3	9.7	9.8	9.9	9.9	10.1	10.4	11.0	11.1	11.1	12.7	12.9	13.2	15.0	18.0	19.0	21.1	21.1	21.1	21.1	21.1	21.1
343	ארני	375	423	713	261	484	1205	1194	742	485	422	1146	1146	732	732	779	1356	640	678	669	669	666	666	627	627
9 -	7	9	10	10			10			9	12		9	9	10	9	9	9	10	9	9	9	9	9	9 [
US-10-119-932-5	TE-00-828-310-12	us-10-119-932-1	US-09-729-674-160	US-09-801-368-408	US-10-132-744A-4	US-10-132-744A-2	US-09-876-667-16	US-09-876-667-2	US-10-077-111-11	US-10-132-744A-6	US-10-042-417-4	US-09-994-485-6	US-09-832-292-10	US-09-832-292-12	US-09-994-485-8	US-10-060-019-29	US-10-077-111-10	US-10-060-019-30	US-09-801-368-314	US-09-328-877A-25	US-09-213-888-25	US-09-328-877A-27	JS-09-213-888-27	JS-09-328-877A-3	US-09-213-888-3
Sequence 5, Appli	Sequence 12. Appl	Sequence 1, Appli	Sequence 160, App	Sequence 408, App	Sequence 4, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 2, Appli	Sequence 11, App1	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 12, Appl	Sequence 8, Appli	Sequence 29, Appl	Sequence 10, Appl	Sequence 30, Appl	Sequence 314, App	Sequence 25, Appl	Sequence 25, Appl	27	Sequence 2/, Appl	ر ا	Sequence 3, Appli

ALIGNMENTS

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; TYPE: PRT; ORGANISM: Homo sapiens
US-10-042-417-2
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US-10-042-417-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
                                                                                                                                                                                                                                                                                                                                                    Matches 569;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-090-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pagano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 569
                                      181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                            181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                      121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
  241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                               61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL 120
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                                                                                                                                                                                           h 100.0%; Score 3034; DB 12; Length 569; Similarity 100.0%; Pred. No. 6.5e-248;
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CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: LASSOT, Irina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA Trcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: BetaTrCP
LOCATION: (1)..(219)
OTHER INFORMATION: F-box protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 219
                                                                       181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKN 219
                                                                                                            181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKN 219
                                                                                                                                                                   121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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                                                                                                                                                                                                                                                                                                    1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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                                                                                                                                              ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                        STAMKTENCVAKTKLANGTSSMIVFKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                               STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                                                                                                                                                                                                                                                                                                                                   38.3%; Score 1163; DB 9; Length 219; 100.0%; Pred. No. 9.6e-91;

 Mismatches

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US-09-213-888-21
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; Sequence 30, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-848-30
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                                                                                                                                                                                                                                                    SEQ ID NO 21
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                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
               Matches 169;
                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PTZO8
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: homo sapien
                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                         LENGTH: 626
TYPE: PRT
                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 53
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         Conservative 103; Mismatches
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                        21.2%; Score 644.5; DB 9; 30.1%; Pred. No. 2.1e-46;
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    222;
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  Indels 67;
                                             Length 626;
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                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: homo sapien US-09-328-877A-21
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                                                                                                                                                                                                                                                                                     SEQ ID NO 21
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                                                                        Matches
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APPLICANT: Pharmacia & Upjoin Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/328,877A CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gurney, Mark E. APPLICANT: Li, Jinhe
                                                                                                                                                                                                       LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHQSLTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGPNKHQSAVTC 548
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                                  LQEKALKEMNSSEREDCHNGEPPRKIIPEK--NSLRQ--TYNSCARLCLNQETVCLASTA 63
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MEQKLISEEDLNEMESLGDLTMEQKLISEEDLNSMKRKLDHGSEVRSFSLGKKPCKVSEY 112
                                                                          169;
                                                                                            Similarity
                                                                        Conservative
                                                                                          21.2%; Score 644.5; DB 9; 30.1%; Pred. No. 2.1e-46;
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                                                                        Mismatches
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                                                                                                            Length 626;
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                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09213888A Patent No. US20020164683A1
                                                                                                                                                                                                                       Matches 167;
                                                                                                                                                                                                                                          Query Match
Best Local
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APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: NENTHON: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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                                                                                                                                                                                                                                                                                                                                           LENGTH: 54
TYPE: PRT
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                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT 73
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                                                           RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 100
                                                                                                 KLANGTSSMIVPKORKLSASYEKEKEL -- CVKYFEOWSESDQVEFVEHLISQMCHYQHGH 131
                                                                                                                                           KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 45
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                                                                                                                                                                                                                     21.1%; Score 640; DB 9; 30.8%; Pred. No. 4.1e-46; ative 92; Mismatches 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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TYPE: PRT
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157 KCKE------EGIDEPLHIKRRK-----VIKPGFIHSPWKSAY-----IRQ--HRI 194
                                              192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI 246
                                                                                               101 MMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE
                                                                                                                                              132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
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                                                                                                                                                                                               46 RAANGQG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 100
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                                                                                                                                                                                                                                                                                               4 KLDHGSEVRSFSLGKKPCKV-----SEYTSTTGL-----VPCSA-----TPTTFGDL 45
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SEQ ID NO 7
LENGTH: 540
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PATENT NO. US20020177187A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
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Best Local :
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APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877A
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
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307 TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
                                                                            195 DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele i
APPLICANT: Pharmacia 6 Up
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ORGANISM: Homo sapiens
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                                                                                                                                                                         195 DTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH
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367 RSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
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APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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LENGTH: 545
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                 487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
                                                              376 QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-328-877A-6
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GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TNURNTION: Human Sel-10 Polypeptides and Polynucleotides that
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LENGTH: 545
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; Patent No. US200201; GENERAL INFORMATION:
                                                                                                              US-09-328-877A-5
                                                                                                                                                              RESULT 13
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                               Sequence 5, Application US/09328877A Patent No. US20020177187A1
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US-09-213-888-5
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APPLICANT: Li, Jinhe
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
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ORGANISM: Homo sapiens
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Sequence 9, Application US/09213888A
Patent No. US20020164683A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
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SEQ ID NO 5
LENGTH: 553
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APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-9
                                                                                                                                                                                                                                     ; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
SOFTWARE:
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Best Local 9
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                                                                                          APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
                                   CURRENT APPLICATION NUMBER: US/09/328,877A CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 27
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Local Similarity 30.8%; Pred. No. 4.3e-46;
nes 167; Conservative 92; Mismatches 211;
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; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877A-9
Search completed: February 20, 2003, 10:00:10 Job time : 17 secs
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                                                                                                                                                                                                           487 AYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFRLQFDEFQIVSSSHDDTILI 543
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 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
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Match
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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Listing first 45 summaries
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US-09-724-676-52733
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US-09-724-676A-52733
US-09-724-676A-52733
US-09-724-676A-61015
US-09-724-676A-61016
US-09-724-676A-61014
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US-09-724-676A-61017
US-09-724-676A-61018
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             61017, A
61018, A
30, Appl
29, Appl
61377, A
61378, A
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61017,
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; OTHER INFORMATION: Description of the artificial sequence ; OTHER INFORMATION: coding for human beta-TrCP protein US-09-601-168B-2 NUMBER OF SEQ ID NOS: 9 SOFTWARE: PatentIn Ver: 2.1 and manually SEQ ID NO 2 LENGTH: 569 APPLICANT: APPLICANT: Query Match Best Local Similarity Matches 569; PRIOR APPLICATION NUMBER: FR98 01100 PRIOR FILING DATE: 1998-01-30 PRIOR APPLICATION NUMBER: FR98 15545 PRIOR FILING DATE: 1998-12-09 CURRENT APPLICATION NUMBER: US/09/601,168B CURRENT FILING DATE: 2000-07-28 PRIOR APPLICATION NUMBER: PCT/FR99/00196 PRIOR FILING DATE: 1999-01-29 FILE REFERENCE: 935. TITLE OF INVENTION: Human beta-TrCP protein APPLICANT: APPLICANT: ORGANISM: Artificial sequence FEATURE: TYPE: PRT 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL 120 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120 KROLL, Mathias CONDORCET, Jean-Paul MARGOTTIN, Florence ARENZANA SEISDEDOS, Fernando Conservative .38812X00 100.0%; Score 3034; DB 5; 100.0%; Pred. No. 5e-273; ative 0; Mismatches 0; Indels Length 569; 0; Gaps

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181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240

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SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 52731
LENGTH: 605
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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)9-724-676-52731
325 SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                         301 ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                          241 GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS 300
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 52731
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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      421 VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
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Similarity 94.08;
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Pred. No. 2.
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GENERAL INFORMATION:
APPLICANT: COMPUSED LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compusen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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TYPE: PRT
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US-09-724-676A-52729
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
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LENGTH: 537
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COURENT APPLICATION NUMBER: US/09,
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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Local Similarity 91.2%;
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; sequence 52729, Application US/09724676A; GENERAL INFORMATION:

APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28

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RESULT 7
US-09-724-676A-52730
Sequence 52730, Appl
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-724-676A-52729
                                                                                                                    APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52730
LENGTH: 537
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ORGANISM: Homo sapiens
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SEQ ID NO 52729
LENGTH: 537
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                              Similarity
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                    89.0%; Score 2701; DB 5; 91.2%; Pred. No. 3.8e-242;
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Pred. No. 3.8e-242;
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                                      DB 5; Length 537;
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; GENERAL INFORMATION
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LENGTH: 573
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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                 85 PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
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                                                                                        25 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETYCLASTAMKTENCYAKTKLANGTSSMIV
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52733
LENGTH: 573
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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Pred. No. 1.7e-239;
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 52732
LENGTH: 573
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 85.8%;
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.7 COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMPUGEN COMP
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Pred. No. 1.7e-239;
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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Pred. No. 1.7e-239;
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 61015
LENGTH: 529
TYPE: PRT
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 61016
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                                                                    Sequence 61015, Application US/09724676A GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER:
               APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVTSDGMLWKKLIERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEP-DSVIEDKTIELMNTSVMEDQNEDESPK-----KNTLWQ------
                                                                                                                                                                                                     ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                        KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLM
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                                                                                                                                                                                                                                                       KRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity

    ISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHL

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.1%; Score 2400; DB 5; 79.3%; Pred. No. 3.3e-214;
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   US/09/724,6762
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US-09-724-676A-61015
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                                              ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676A-61016
                                                                                                                                                                                                                                                              ; Sequence 61016, Application US/09724676A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 US-09-724-676A-61016
                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                               APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 61016
LENGTH: 529
TYPE: NEWSTH. 529
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LENGTH: 529
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Query Match
Best Local Similarity
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                             ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEP-DSVIEDKTIELMNTSVMEDQNEDESPK-----KNTLWQ----
                                                                                                                                                                                                                                                                                                                                                                         ILIWDFLNVPPSAQNETRSPSRTYTYISR 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLM 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHL
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NOS: 97222
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79.1%;
79.3%;
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 Score
Pred.
 2400; DB 5;
No. 3.3e-214;
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	ILINDELNVPPSAQNETRSPSRTYTYISR 529	Db 501	
	ILIWDFLADPAAQAEPPRSPSRTYTYISR 569	Qy 541	
	KRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDT 500	Db 441	
	KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540	Qy 481	
	EFVRTLNGHKRGIACLQYRDRLYVSGSSDNTIRLMDIECGACLRVLEGHEELVRCIRFDN 440	Db 381	
	EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480	Qy 421	
	VTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTC 380	Db 321	
	VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC 420	0у 361	
·	KVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLM 320	Db 261	
	RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRENNGMM 360	Qy 301	
	QDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECL 260	Db 201	
	QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300	Qy 241	
	RVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKII 200	Db 143	
	RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240	Qy 181	
	ISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQ 142	Db 83	
	ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180	Qy 121	
	ISNGTSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHL 82	Db 37	
	STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120	Qy 61	
	MEP-DSVIEDKTIELMNTSVMEDQNEDESPKKNTLWQ 36	Db 1	
	(IIPE	Ωу 1	
4;	451; Conservative 43; Mismatches 35; Indels 40; Gaps	Matches	

Search completed: February 20, 2003, 09:59:48
Job time: 59 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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3034
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Listing first 45 summaries
// Cgn2_6/ptodata/1/paa/US084_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US085_COMB.pep: *
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// Cgn2_6/ptodata/1/paa/US087_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US089_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US099_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US099_COMB.pep: *
// Cgn2_6/ptodata/1/paa/US093_COMB.pep: *
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// Cgn2_6/ptodata/1/paa/US096_COMB.pep: *
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Copyright (c) 1993 - 2003 Compugen Ltd.
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'Cgn2_6/ptodata/1/paa/US07_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US080_COMB.pep:*
'Cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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2462.102 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

Result No.	Score	⊃~	Length DB ID	DB	ID	Description
1	3034	100.0	569	- 3	PCT-US02-00311-2	Sequence 2, Appli
2	3034	100.0	569	ᆫ	PCT-US99-19560-2	Sequence 2, Appli
ω	3034	100.0	569	16	US-09-210-060-18	Sequence 18, Appl
4	3034	100.0	569	17	US-09-385-219-2	Sequence 2, Appli
ر د	3034	100.0	569	18	US-09-415-795-4	Sequence 4, Appli
6	3034	100.0	569	18	US-09-455-371-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
PCT-US02-00311-2
PCT-US02-00311-2
PCT-US02-00311-2
PCT-US02-00311-2
PCT-US02-00311-2
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PCT-US02-00311-2
PCT-US02-00311
PCT-US02-00311
PCT-US02-00311
PCT-US02-00311
PROBLETION NUMBER: PCT/US02/00311
PTILE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
PILE REFERENCE: 5914-090-228
PCURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: PCT/US02/00311
CURRENT FILING DATE: 2001-01-5
PRIOR FILING DATE: 2001-01-5
PRIOR FILING DATE: 2001-01-5
PRIOR PILING DATE: 2001-01-5
PRIOR PRIOR PATENTIN VET. 2.0
PRIOR FILING DATE: 2001-01-5
PCT-US02-00311-2
PCT-US02-00311-2

Query Match
PCT-US02-00311-2

Query Match
Pest Local Similarity 100.0%; Score 3034; DB 1; Length 569;
PCT-US02-00311-2

Query Match
Pest Local Similarity 100.0%; Pred. No. 1.3e-284;
Matches 569; CONSETVATIVE 0; MISMATCHES 0; Gaps 0;
MISMATCHES 569; CONSETVATIVE 0; MISMATCHES 0; MISMA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NEW YORK UNIVERSITY
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC
FILE REFERENCE: 5914-081-228
CURRENT APPLICATION NUMBER: PCT/US99/19560
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: 60/98,355
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1999-02-03
EARLIER FILING DATE: 1999-02-03
EARLIER FILING DATE: 1999-02-03
                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/124,449
EARLIER FILING DATE: 1999-03-15
NUMBER OF SEO ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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SEQ ID NO 18
: LENGTH: 569
: TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION TITLE OF INVENTION: NF-kB FILE REFERENCE: 860098.427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lavon, Iris
APPLICANT: Yaron, Avraham
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181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
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                                        ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
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APPLICANT: Chiaur, D.
APPLICANT: Pagano, M.
APPLICANT: Pagano, M.
APPLICANT: Pagano, M.
APPLICANT: Latres, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS
FILE REFERENCE: 5914-081
CURRENT APPLICATION NUMBER: US/09/385,219
CURRENT FILING DATE: 1999-08-27
EARLIER APPLICATION NUMBER: 60/098,355
EARLIER APPLICATION NUMBER: 60/118,568
EARLIER APPLICATION NUMBER: 60/118,568
EARLIER APPLICATION NUMBER: 60/124,449
EARLIER FILING DATE: 1999-02-03
EARLIER FILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
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Best Local S
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ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
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Similarity 100.0%; Pred. No. 1.3e-284;
69; Conservative 0; Mismatches 0;
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APPLICANT: Zhou, Pengbo
APPLICANT: HowLey, Peter M.
TITLE OF INVENTION: TARGETED PROTEOLYSIS BY
TITLE OF INVENTION: PROTEIN LIGASES
FILE REFERENCE: HMV-043.01
CURRENT APPLICATION UNMBER: US/09/415,795
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 47
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SEQ ID NO 4
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Pred. No. 1.3e-284;
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APPLICANT: Winston, Jeffrey T.
APPLICANT: Winston, Jeffrey T.
APPLICANT: Winston, Jeffrey T.
APPLICATION: Regulation of I Kappa B (IK-B) Degradation and Methods and Reagen
TITLE OF INVENTION: Related Thereto
FILE REFERENCE: 12541-1010
CURRENT APPLICATION NUMBER: US/09/455,371
CURRENT FILING DATE: 1999-12-03
PRIOR FILING DATE: 1998-12-03
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APPLICANT: Elledge, Stephen
APPLICANT: Harper, J. Wade
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                                                                                       RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
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SEQ ID NO 2
LENGTH: 569
TYPE: PRT
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Best Local
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Harper, J. Wade
Rolf, Mark
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APPLICANT: Strack, Peter J.

APPLICANT: Winston, Jeffrey T.

TITLE OF INVENTION: Regulation of I Kappa B (IK-B) Degradation and Methods and Rea

TITLE OF INVENTION: Related Thereto

FILE REFERENCE: 120541-1010

CURRENT APPLICATION NUMBER: US/09/455,371B

CURRENT FILING DATE: 1999-12-03
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PRIOR APPLICATION NUMBER: PCT/FR99/00196
PRIOR ETLING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: FR98 01100
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-12-09
PRIOR FILING DATE: 1998-12-09
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ORGANISM: Artificial sequence
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CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 60/085,3434; 60/098,010

PRIOR FILING DATE: 1998-05-13; 1998-08-26
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APPLICANT: BAUGHN, Mariah R.
APPLICANT: YANG, Junning
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TYPE: PRT
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LENGTH: 569
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APPLICANT: Dobe, Derek
APPLICATION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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SOFTWARE: PatentIn Ver.
SEQ ID NO 18
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/210,060
PRIOR FILING DATE: 1998-12-10
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APPLICANT: Mercurio, Frank
APPLICANT: Amit, Sharon
APPLICANT: Ben-Neriah, Yinon
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TYPE: PRT
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                   481 KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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Yaron, Avraham
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FEATURE:

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LOCATION: (1)..(569)

OTHER INFORMATION:
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APPLICANT: Pierre, Legrain
TITLE OF INVENTION: Protein-protein interactions
FILE REFERENCE: B4767A
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                       KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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Sequence 2, Application US/10042417
GENERAL INFORMATION:
APPLICANT: PAGANO, M.
TITLE OF INVENTION: METHODS TO IDEN
TITLE OF INVENTION: PROLIFERATIVE
FILE REFERENCE: 5914-090-999
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local
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CURRENT APPLICATION NUMBER: US/10/042,417
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-5
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TYPE: PRT
ORGANISM: Homo:
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US-60-098-010-5
; Seguence 5, Application
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Tang, Y. Ton

Application US/60098010

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Sequence 2, Application US/60098355
GENERAL INFORMATION:
APPLICANT: Chiaur, Dah Shiarn
APPLICANT: Pagano, Michele
APPLICANT: Lattes, Esther
TITLE OF INVENTION: NOVEL UBIQUITI
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LENGTH: 569
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APPLICANT: Lal, Preeti
APPLICANT: Baughn, Mariah R.
APPLICANT: Patterson, Chandra
APPLICANT: Quegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: G-PROTEIN SIGNALING PATHWAY MOLECULES
FILE REFERENCE: PF-0583 P
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CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 12
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ORGANISM: Homo sapiens
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AS THERAPEUTIC
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Search completed: February Job time : 151 secs

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; ORGANISM: HUMAN
US-60-098-355-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/098,355
CURRENT FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 3034; Best Local Similarity 100.0%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 5914-070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 569
                                541 ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                             VTCSKDRSIAVMDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMNTSTC 420
                                                                                     KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
ILIWDFLNDPAAQAEPPRSPSRTYTYISR
                                                                                                                                                            EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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                                                                    KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                         EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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1.3e-284;
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Listing 1...

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
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     // SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
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881.623 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	9	6 0	7	σ	տ	4	ω	2	1	Result
2997	3006	3027	3027	3034	3034	3034	3034	3034	3034	Score
98.8	99.1	99.8	99.8	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
569	605	809	569	569	569	569	569	569	569	Query Match Length DB
21	22	22	22	21	21	21	21	21	20	DB
AAB12812	AAM78582	AAM00960	AAB48298	AAY44249	AAY83250	AAY83041	AAY96697	AAB12813	AAY24054	ID
Mouse ubiquitin in	Human protein SEQ	Human bone marrow	Human ZF11 protein	Human cell signail	F-box protein neet	F-box protein FBP-	Human beta-TrcP.	Human beta-transdu	A human beta-trans	Description

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45	44	43	42	41	40	39	38	37	36	ω	34	ω ω	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11 ·
640	640	640	640	640	640	640	640	640	640	640	640	640	640	644.5	644.5	661	661	661		989.5	1163	2089.5	2384.5	2384.5	2384.5	2384.5	2582.5	2882	2962	2989.5	2989.5	2989.5	2992.5	9
21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.2	21.2	21.8	21.8	21.8	30.8	32.6	38.3	68.9	78.6	78.6	78.6	78.6	85.1	95.0	97.6	98.5	98.5	98.5	98.6	98.8
589	589	589	559	559	553	553	553	545	545	540	540	540	540	626	626	1326	1326	1326	448	265	219	510	550	542	542	542	517	579	590	654	654	654	632	569
22	21	20	22	20	22	22	20	22	20	22	22	20	20	22	20	22	22	22	22	22	23	22	22	22	22	21	16	22	22	22	22	22	22	21
AAB59198	AAB01204	AAY22466	AAB59199	AAY22467	AAB59195	AAB93475	AAY22463	AAB59196	AAY22464	AAB59200	AAB59197	AAY22468	AAY22465	AAB59201	AAY22469	ABB70051	ABB67238	ABB67237	AAB48289	AAU86942	AAU98087	ABB59857	AAM41994	AAM40208	AAM79127	AAY96696	AAR85852	AAM78583	AAM00847	AAM79568	AAM79567	AAM79566	AAM78584	AAY83254
Human mammary sel-	Human GTPase assoc	Human mammary sel-	Human mammary sel-		Human hippocampal	Human protein sequ	Human hippocampal	Human hippocampal	Human hippocampal	Human mammary sel-	Human hippocampal	Human mammary sel-	Human hippocampal	Protein encoded by	Human 6myc-N-sel-1		Drosophila melanog		Beta-TRCP.N/SKP2.C	Human DNA repair a	Human beta TrCP (b	Drosophila melanog	Human polypeptide	Human polypeptide	Human protein SEQ	Human E3 ubiquitin	WD-40 domain-contg	Human protein SEQ	Human bone marrow	Human protein SEQ		protein		protein

ALIGNMENTS

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RESULT 1 AAY24054 AAY24054; AAY24054 standard; Protein; 569 AA. 30-SEP-1999 (first entry)

A human beta-transducin repeat containing protein.

Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Vpu protein; beta-catenin; human immune deficiency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation; tumour necrosis factor

Homo sapiens.

Region	Region	Region	Region	Region	Key Region
427455 /note= "WD motif"	387415 /note= "WD motif"	/note= "WD motif"	/note= "WD motif"	/HOLE F DOX SEQUENCE 259292 /note= "WD motif"	Location/Qualifiers

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CC protein (beta-TrcP). The protein directs proteins to the proteosome CC protein (beta-TrcP). The protein is able to interact with the Vpu CC protein of human immune deficiency virus! (HIV-1), cellular proteins CC ubiquitinylation of phosphorylated protein skplp. The protein controls CC ubiquitinylation of phosphorylated proteins and thus their targeting to CC inhibited or promoted, the result may be delayed breakdown of CD4 (in CC cases of HIV-1 infection); increased activity of IKB (and thus reduced CC calls, or increased be survival (and reduced apoptosis) in Alzheimer's CC patients. The beta-TrcP protein, and its active peptide fragments, or its CC culsic acid, are used to screen for anti HIV-1 agents (antivirals), CC degradation in human tumour cells, and anti-inflammatory agents that CC cuseful for treating osteo-articular inflammation or acute inflammation or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated with release of tumour necrosis factor.
241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                       241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQVDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human beta-transducin repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 60-61; 71pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory and anti-Alzheimer's agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human beta-transducin repeat containing protein and its fragments useful as, or to screen for, antiviral, antitumour.
                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX86501
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDPAEAVLOEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                              RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                              RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                                                                                                                                                                              STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL 120
                                                                                                                                                                                             ISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                               ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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Query Match Best Local Similarity

100.0%; Score 3034; DB 21; 100.0%; Pred. No. 1.4e-286;

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                        The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12B13, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
Sequence
                                                                                                                                                                                                              Claim 3; Page 10-12; 19pp; Japanese.
                                                                                                                                                                                                                                               F\text{-}box\ protein\ of\ ubiquitin\ ligase\ SCF\ complex\ which\ promotes\ the\ ubiquitination\ of\ IKappaB\ or\ beta-catenin\ .
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA73132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; FWD1; gene _therapy; colon cancer; beta-transducin repeat containing protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta-transducin repeat containing protein (beta-TrCP) SEQ ID NO:3
                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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DRX PRACTICAL AND CONTRACT CON
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Lavon I,
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                                                                                                                             (SIGN-)
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Polypeptide enhancing phosphorylated lkappaB ubiquitination treating disorder associated with NF-kappaB activation e.g. comprising amino acid sequence of human E3 ubiquitin ligase
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Claim 21; Page 72-74; 77pp; English.

Human beta-TrCP, an F-box/WD protein family member, has been shown to have homology to human E3 ubiquitin ligase (B3). E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying modulators of this process for use in treating diseases associated with activation of NF-kappa-B. In vitro analysis suggests that deletion of the F-box results in a protein that functions as a dominant negative molecule in vivo. Transient over-expression of delta-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha activity. E3 and beta-TrCP can be used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections.

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              ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                           KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiaur DS,
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 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
              RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
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                                                                                                                     STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is
                                                                                                                                                                                                                    Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with undiquitin protein ligase or inhibiting ubiquitination using organic
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                                                         Cell signalling protein-12; CSIGP-12; cell proliferation; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; arteriosclerosis; Addison's disease; multiple sclerosis.
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Human cell signaling proteins useful for, proliferative and inflammatory disorders

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                                                02-APR-2001
                                                                                      AAB48298;
                                                                                                                        AAB48298 standard;
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                                                                                                                                                                                                           ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                (first entry)
                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Addison's disease, multiple sclerosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3034; DB 21; Pred. No. 1.4e-286;
                                                                                                                      B
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EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN

VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC

VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC

RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM

RILTGHTGSVLCLQYDGRVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM

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                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/CDC53 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 130-132; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC84610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-2000; 2000WO-US15449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-phase kinase associated protein; SKP1; SKP2; CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYYA ) UNIV YALE
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     241
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                                                                                                                                                                                                                         61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                       1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETYCLA
                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                     1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                                                                                      RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                    RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                    ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                    STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                    ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-061703/07
                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         569 AA;
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                          99.8%;
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                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKP2-like protein; c-Myc; MDM2; p53; F
                                                                                                                                                                                                                                                                                                                                                                      Length 569;
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow; antiinflammatory; cytostatic; neuroprocessantiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; coell differentiation modulator; HIV; autoimmune disorder; haemo
          be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                           The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may
                                                                                                                                                                                                                                     Claim 10; Page 523-524; 648pp; English.
                                                                                                                                                                                                                                                                  Novel bone-marrow-expressed polynucleotides and for treating e.g. cancer and immune deficiency of
                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow protein,
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                                                                                                                                                                                                                                                                                                                                                          JE,
Wang
                                                                                                                                                                                                                                                               treating e.g. cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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bB; AAH90079.
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Wang J, Wer
Zhou P, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0552317
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                                                                                                                                                                                                                                                                                                                                                                      Werhman
                                                                                                                                                                                                                                                                                                                                                     J, Tang YT,
Werhman T, XI
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; neuroprotective;
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ie AJ, Yang
                                                                                                                                                                                                                                                                  d polypeptides, useful disorders -
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Y, Z
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 Matches 567;
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03-FEB-2000;
27-APR-2000;
20-JUN-2000;
                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                 AAM78582
                                                                                                                                                                                                                                Human protein SEQ ID NO 1244.
                                                                                                                                                                                                                                                            06-NOV-2001
                                                      05-FEB-2001;
                                                                                 09-AUG-2001.
                                                                                                           WO200157190-A2
                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
; 2000US-0496914.
; 2000US-0560875.
; 2000US-0598075.
                                                    2001WO-US04098
                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.88;
                                                                                                                                                                                                                                                                                                                 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinyinhibin activity and may be useful in the diagnosis and/or reatment of cancer lenvisories are content in the diagnosis and/or reatment of cancer lenvisories.
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15-SEP-2000;
20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 3503-3504; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with useful in diagnosis and gene therapy -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                          VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
                                                             SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR 384
                                                                                                                             ETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
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                                                                                                                                                                                                           GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS 264
                                                                                                                                                                                                                                                                                                                                                 PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              605 AA;
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94.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and wp40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin repeat containing protein (beta-TrCP)). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-box protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin -
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
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STAMKTENCVAKAKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                               STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                                                                                                                                                                                                                                                             destabilisation; proteolysis; drug discovery; gene oncoprotein; Huntington's disease; gene knockout; d
                                                                                                                                                                                                                                                                                                                                                   Ubiquitin ligase; SCF; F-box protein; targeted degradation;
                                                                                                                                                                                                                                                                                                                                                                            F-box protein FWDlp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY83254 standard;
                                                                Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                       08-OCT-1999;
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                                 Claim 9; Page 184-185; 185pp; English.
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                                                                                                                                                   P, Howley P;
                                                                                                                             2000-317970/27.
                                                                                                                  AAZ93714.
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                                                                                                                                                                                                 98US-0103787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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delivery systems;
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The F-box proteins ligases) which can

are a family of ubiquitin be used for the targetted

ligases (SCF ubiquitin degradation of a targe

RESULT 12 AAM78584

AAM78584 standard; Protein; 632

XEXEXEX

06-NOV-2001

(first entry) SEQ ID NO 1246

Human protein

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                                                                                    KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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                                                                                                                                                           EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLMDIECGACLRVLEGHEELVRCIRFDN
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                                                                                                                                        EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
ILIWDFLNDPAAHAEPPRSPSRTYTYISR 569
                                                                   KRIVSGAYDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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98.6%;
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Pred. No. 5
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5.8e-283;
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Best Local
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01-SEP-2000;
15-SEP-2000;
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Zhao QA,
                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like
                                                                                                                                                                                                                                                                                                                                 (AAM80020) are omitted as the relevant pages from the wore missing at the time of finitiantian.
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30-NOV-2000;
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20-JUN-2000;
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EHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 177
                                                           CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV
                                                                         CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117
                                                                                                                 MPSLRCLYNPGTGALTAFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 120
                                                                                                                                                                                                           MDPAEAVLQEKALK-----
                                                                                                                                                                                                                                                                                                                              missing at the
                                                                                                                                                                           MDPAEAVLQEKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT, Asundi V, Zhou
Wang D, Wang J, Zhang J, Ren F, (Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                  632 AA;
                                                                                                                                   -----FMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 57
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2000US-0560875.
2000US-058075.
2000US-0520325.
2000US-0620325.
2000US-063936.
2000US-063325.
2000US-063325.
2000US-0728422.
                                                                                                                                                                                                                                                                                                                           time of publication.
                                                                                                                                                                                                                                                    98.6%;
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Pred. No. 1.9e-282;
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Zhao QA,
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                           WPI; 2001-476283/51.
N-PSDB; AAK52699.
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                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYP
                                                                                                                                                                                                                                                                                                                                                                              cytokine;
                                                                           Yang Y,
                                                                                                                                                                                                                                                                                                                                                   ytokine; cell proliferation; cell differentiation; gene therapy; peptide therapy; stem cell growth factor; haematopoiesis; rowth factor; immunomodulatory; cancer; leukaemia;
                                                                                      Wang
                                                                                                 Liu C,
                                                                                                                                            2000US-0496914.

2000US-0560875.

2000US-0598075.

2000US-0598075.

2000US-0620325.

2000US-0634936.

2000US-063325.

2000US-0693325.

2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                         disorder; arthritis; inflammation.
                                                                          Drmanac RT, Asundi V,
, Wang J, Zhang J, Ren
Wejhrman T, Goodrich R,
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                                                                                     Zhou
                                                                                     Chen
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                                                                                     , Cao Y,
Wang ZW;
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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
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                                   AAM79567 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117
                                                                                                                                                                                GMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPSLRCLYNPGTGALTAFQNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDPAEAVLQEKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS
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                                                                                                                                                                                                                                                                                                                                                                                                              ECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV
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                                                                                                                                                DDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                               STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
                                                                                                                                                                                                                                                                              STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
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                                  Protein;
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89.9%;
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Pred. No. 3.9e
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3.9e-282;
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                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or activity, inhibit activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT, Zhao QA, Wang D, Wang J, Z Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                     treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                          inflammation
143 CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV
               58 CLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFV 117
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                                                                                                                                                                                                 Local Similarity
                                                                                                                                                     1 MDPAEAVLQEKALKFM------
                                                             MPSLRCLYNPGTGALTAFQNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV 142
                                                                                                                        MDPAEAVLQEKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS
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                                                                                          20; Page 286; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids encoding polypeptides with in diagnosis and gene therapy -
                                                                                                                                                                                                                                              654 AA;
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2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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89.9%;
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                                                                                                                                                                                                 Score 2989.5; DB 2
Pred. No. 3.9e-282;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine-like activities
                                                                                                                                                                                                               DB 22; Length 654;
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R, Wang ZW;
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N-PSDB; AAK52701.

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27-APR-2000;
20-JUN-2000;
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20-OCT-2000;
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                                                   Xue АJ,
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2000US-0560875.
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2000US-0634936.
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2000US-0728422.
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                                              Drmanac RT, Asundi V, Zhou, Wang J, Zhang J, Ren F, (Wejhrman T, Goodrich R;
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Matches 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78823-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity, insurance control to the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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DDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                             FDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSH
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                                                                            FDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSH
                                                                                                                                                                                   STCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIR
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Search completed: February 20, 2003, 09:53:46 Job time : 89 secs



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Post-processing: Minimum Match 0%
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3034
1 MDPAEAVLQEKALKF
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Match
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LI23_CAEEL
POFB_SCHPO
POFI_SCHPO
SCOB_EMENI
MT30_YEAST
SCO2_NEUCR
SC10_CAEEL
HET1_PODAN
POP1_SCHPO
CC4_YEAST
POP2_SCHPO
CC4_YEAST
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!- ALTERNATIVE PRODUCED BY !- SIMILARITY: !- SIMILARITY:	SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGAS SUBCELLULAR LOCATION: Cytoplasmic.		eta-catenin and stimulates i-kappa-s-aipna ubiquitina enes Dev. 13:270-283(1999).	ted destruction motifs in I-kappa-B-alpha and	er J.W.;	<pre>Minston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,</pre>		9:1177-1179(1999).	Pagano M.; "Identification of a family of human F-box proteins.";	Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,	SEQUENCE FROM N.A. (ISOFORM 2). N. MEDLINE=20003060: PubMed=10531035;	[3]	pacitway cittodyn an r-box mocti.	ein, h-beta TrCp, that interacts with		; PubMed=9660940;	TISSUE-Lymphoid;	115050	Nature 396:590-594(1998). 766,10	ceptor	ercurio F., Ben-Neriah Y.,	PubMed=9859996; A. Davis M. Lavon I., Amit S	SEQUENCE FROM N.A. (ISOFORM 1).		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	nists. Vortobrata.	(ESRSIKAPPAB) (PIKAPPABAIPHA-ES FECEPLOF SUBURIL). FBXWIA OR FBWIA OR BTRCP OR BTRC.	F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP)	Last	(Rel. 40, Creat	FWIA_HUMAN STANDARD; PRT; 605 AA.	LT 1 _HUMAN

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SEQUENCE
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PROSITE; PS00678; WD_REPEATS_1; 6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00400; WD40; 'Pfam; PF00646; F-box;
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PAN 199

PEAT 341

PEAT 381

PEAT 424

PEAT 462

PEAT 505

PEAT 553
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              VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV 444
 VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV
                                                                                                                           ETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                 GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                     {\tt SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR}
                                                                       SDSTVRVWDVNTGEMLNTL1HHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                                                           ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                                           GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                                                                                                       ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
                                                                                                                                                                                                                                                                                              PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
                                                                                                                                                                                                                                                                                                                                 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV
                                                                                                                                                                                                                                                                                                                                                 NNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLANGTSSMIV
                                                                                                                                                                                                                                                                                                                                                                                       MDPAEAVLQEKALKFMCSMPRSLWLGCSSLADSMPSLRCLYNPGTGALTAFQNSSEREDC
                                                                                                                                                                                                                                              ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR 204
                                                                                                                                                                                                                                                                           PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   569;
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SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:1144; BTRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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94.0%;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
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Pfam; PF00400; WD40; 7 Pfam; PF00646; F-box;

PD000018; WD40; PR00320; GPROTEINBRPT InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.

EMBL; M98268; AAA02810.1; -. EMBL; U63921; AAB49671.1; -. EMBL; U63922; AAB49672.1; -.

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                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differential display PCR.";
Dev. Genet. 19:190-198(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE-93330289; PubMed-8393141; Spevak W., Keiper B.D., Stratowa C., Castanon M.J.; Spevak W., Keiper B.D., Stratowa C., Castanon M.J.; "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein with heta-transducin repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91854; P70037; P70038;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 302-518 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBXW1 OR BTRCP.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-TrCP (Beta-transducin repeat-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Probably recognizes and binds to some phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Identification of new localized RNAs in the Xenopus oocyte by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ludson J.W., Alarcon V.B., Elinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97109804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRCB_XENLA
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                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 7 WD REPEATS (TRP-AS SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE-
MATURED OCCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins and promotes their ubiquitination SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX)
                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                TADPOLE EMBRYO.
                                                                                                                                                                                                                                                                                                                                                            NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beta-transducin repeats.";
Cell. Biol. 13:4953-4966(1993).
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RESULT 3
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ID FWLB H
AC Q9UKB1
DT 16-CCT
DT 15-JUN
DE F-box/
GN FBXMLB
OS HOMO S
OC Manmal
OX NCBL_T
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Matches 488
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DOMAIN 119
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                                       Q9UKB1; Q9Y4C6; Q9P2S8; Q9P2S9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
F-box/MD-repeat protein 1B (F-box and MD-rej
FBXM1B OR FBW1B OR BTRCP2 OR KIAA0696.
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          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         163
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                                                                                                  HUMAN
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                                                                                                                                                                                                      YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
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                                                                                                                                                                                                                                             TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSTCEFVRTLNGHKRGIACLQ
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SM00320;
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516
518 /
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WD40; 7.
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                                                                                                   STANDARD;
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91.6%;
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Pred. No. 3
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A -> AAH (IN REF. 2).
2A52EC19028127F3 CRC64;
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                                                  WD-repeats
                                                             update)
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3.9e-188;
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                                                    beta-TrCP2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Ubl conjugation | 129 | 129 | REPEAT | 238 | REPEAT | 278 | REPEAT | 318 | REPEAT | 401 | REPEAT | 402 | REPEAT | 442 | REPEAT | 442 | REPEAT | 490 | REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-20003060; PubMed=10531035;
Cenciarelli C., Chiaur D.S., Guard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMPL outstation its suspense Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal lung
MEDLINE=20160458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           code for large proteins in vitro on Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Prediction of the coding sequences of The complete sequences of 100 new cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 5q35.1."
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Katoh M.;
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                                                                                                                                                                                                                                                                 PROSITE; PS50181; FBOX; 1. 5.
PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_REGION;
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT
ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001810; F-b
InterPro; IPR001680; WD4
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
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  VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98403880; PubMed-9734811;
Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and genomic structure of the betaTRCP2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation. SUBBUNIT: PART OF A SCF (SKP1-GULINI-F-BOX) PROTEIN LIGASE COMPISUBCELLULAR LOCATION: Cytoplasmic (Potential). ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AND C (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. PROBUCED BY ALTERNATIVE SPLICING. SIMILARITY: CONTAINS 1 F-BOX DOMAIN. SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w; HGNC:13607; FBXW1B. 605651; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB033281; BAA92331.1; -.
AB014596; BAA31671.1; ALT_INIT.
PubMed=10694485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD40.
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                                                                                                                                                                                                                       Repeat; WD F-BOX.
                    WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
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WD 7.
WD 7.
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  CSVPRSLWLGCANLVESMCALSCLQSMPSVRCL
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                                                                                                                                                                                                                                                 repeat;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                      L123_CAEEL STANDARD; PRT; (09990; O9GNN6; 15-JUL-1998 (Rel. 36, Created) 15-JUN-2002 (Rel. 41, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation
                      Submitted
                                        Miller N.
                                                                 SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                    Kipreos B.T., Gohel S.P., Hedgecock E.M.;
"The Caenorhabditis elegans F-box/WD-repeat protein
to limit cell division during development.";
Development 127:5071-5082(2000).
                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL MEDLINE=20515608; PubMed=11060233;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLKVLTGHTGSVLCLQYDERVIVTGSSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNGFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIQDIETIESNWRCGRHSLQRIHCRSETSKGYYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WQRVISEGMLWKKLIERMYRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S--TAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCLQSMPSVRCL---QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVE
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               (JUN-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                             Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches
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No. 4.1e-172;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
SMART; SM00256; WD40; 7.
SMO320; WD40; 7.
SMO320; WD40; 7.
SMO31TE; PS50181; FBOX; 1.
SMO31TE; PS00678; WD_REPEATS_1; 5.
SMO31TE; PS00678; WD_REPEATS_2; 7.
SMO31TE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
DOMAIN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; K10B2.1; CE28600.
InterPro; IPR001810; F-box
InterPro; IPR001680; WD40.
Pfam; PF00440; WD40; 7.
Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
REVISIONS
                                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U28730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted -!- FUNCT!
248 SNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHT
                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston
                                                                                                                                                      87
                                                                                                                                                                                                                                      27 KPLSIDYLQGHEGLIEEVLKWSEHEQLDFMDKIVHRLSHYQLGKVDNFIRPMLQRDFISN
                                                                                                                                                                                                                                                                                   88 RKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 7 WD REPEATS (TRP SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
DEVELOPMENTAL STAGE: Highest levels in embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 F-BOX DOMAIN. SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: Functions cell autonomously to negatively regulate cell cycle progression. Required to restrain cell proliferation in
                                                                                                                                              LPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGQHWKKLIEKNVRSDSLWWGLS
                                                                                                                                                                                      LPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLA
                                               EKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKLYPKIIRDIHNID
                                                                                                    ERRGWGQYL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response to developmental cues. Probably recognizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   levels in larvae. Maternal expression
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                                                                                                                                                                                                                                                                                                                                               316;
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         665 AA;
                                                                                                                                                                                                                                                                                                                                            Conservative
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127
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63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         75916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WI
F-BOX
                                                                                                                                                                                                                                                                                                                                            59;
                                                                                          -----FKNKPPDGNAPPNSFYRALYPKIIQDIETIE
                                                                                                                                                                                                                                                                                                                                                                                         Score 1638.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALA-RICH.
G->R: IN LIN-32(RH293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD 5. WD 7.
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                                                                                                                                                                                                                                                                                                                                                                   No. 7
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RA Wood V, Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McLean J.,
RA James K., Jones M., Leather S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Moodward J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rleger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POFB_SCHPO STANDARD;
Q09855; Q9P7V1;
01-FEB-1996 (Rel. 33, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F-box/WD-repeat protein pofil. POFIL OR SPAC30.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Harrison C.L., Toda T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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SMART; SM00320; WD40; 8.
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Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
PRINTS; PR00320; GPROTEINBRPT
PRODOM; PD000018; WD40; 3.
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InterPro; IPR001680;
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                                                YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
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                                                                                                                                                        ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                                                                                                                           SGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
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                                                                                                                                                                                                                                                                                                                   RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV
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498 VAALDPRAPAGTLCLRTLVEH------SGRVFRLQFDEFQIVSSSHDDTILIWDF 546

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RX MEDLINE-2184401; PubMed=11859360;
RX MEDLINE-21848401; PubMed=11859360;
RA MOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sqouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R., Fritzc C., Holzer E., McBert T., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft M., Muller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft M., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moseft M., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jinenez J., Sanchez M., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jinenez J., Sanchez M., del Rey F., Benito J.,
RA Daga R.R., Cruzado L., Jinenez J., Sanchez M., del Rey F., Benito J.,
RA Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;
REL Nature 415:871-880(2002).
CC - FUNCTION: Probably recognizes and binds to some phosphorylated
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-box/WD-repeat protein pof1 (Skpl-binding protein 1).
POF1 OR SBP1 OR SPAC57A10.05C.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                     -i-FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katayama S., Kitamura K., Toda T.;
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                                                                                                                                                                                                                                     (BY SIMILARITY).
SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                            proteins and promotes their ubiquitination and degradation. SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497
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AB032410; BAA84528.1;
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15-JUL-1998 (Rel. 3 15-JUL-1998 (Rel. 3 16-OCT-2001 (Rel. 4 Sulfur metabolite r

(Rel. 36, Created)
(Rel. 36, Last sequence update)
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RESULT 7
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Best Local
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ProDom; PD000018; WD40; 5.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 --- CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 RIHCR----SETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 VRTDSLWRGLAERRGWGQYLFKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 DSLVRLDFLSLLPV----EISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQH 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 SSMIVPKQRKLSASYEKEKELCVKYFEQWSE----SDQVEFVEHLISQMCHYQHGHINSYL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL 101
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MAIN 107 153
SPEAT 271 299
SPEAT 311 339
SPEAT 350 379
SPEAT 390 420
KVWEACE-----CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP
                                                     KVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                     VQSLALADSRLFSCSLDGTIKQWDIEKKKCVHTLFGHIEGVWEIAADHLRLISGAHDGVV
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                                                                                                                                                                                                                                                                                                                                                            FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF
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                                                                                                                                                                              IACLQYRDRLYVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
                                                                                                                                                                                                                                   SGGKRITLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTFSAHIGP 436
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F-BOX.
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WD 5.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U21220; AAC15905.1; -. InterPro; IPR001810; F-box. InterPro; IPR001680; WD40.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franscription
                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                       LQGIMAQCCFPQLSYISATVRDLIRIDFITALP----PEIAFKILCYLDTTSLCKASQVS 208
TETGEELRTLRGHESGIRCLQFDDTKLISGSMDRTIKVWNWRTGECISTYTGHRGGVIGL 435
                                               KNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHL 353
                                                                                                                                                    KIIQDIETIESNWRCGRHSLQRIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWD
                                                                                                                                                                                                      DKGVVGPRSPDASAESPPSGKRKLEDDEVAVVKRHCSSLGSDAGVDKDSDFFKTRYRPWK
                                                                                                                                                                                                                                                        -----PPDGNA--PP-----P 237
                                                                                                                                                                                                                                                                                                        RGWRALADDDVVWHRMCEQHIHRK-----CKKCGWGLPLLDRKRLRESKREIELRATTW 262
                                                                                                                                                                                                                                                                                                                                                          KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNK------
                                                                                               EVYKDRFKVGTNWKYGR-----CSIKTFKGHTNGVMCLQFEDNILATGSYDTTIKIWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00256; FBOX;
SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50181; FBOX; 1.
PS00678; WD_REPEATS_1; 4.
PS50082; WD_REPEATS_2; 7.
PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α.
Έ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76070 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.0%; Score 575; DB 1; 26.9%; Pred. No. 9.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D840D452E37B4C53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the EMBL outstation are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 678;
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밁
                                                                                                                                                                                                                                                                                    Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                         modified and this statement is not removed. Usage by and for common send an email to license@ieh---
                                                                                                                                                                                                             GENES EXPRESSION.
-!- SUBUNIT: SEEMS TO INTERACT WITH MET4.
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TEP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TEP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        adenosylmethionine, is an essential protein with WD40 repeats."; Mol. Cell. Biol. 15:6526-6534(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surdin-Kerjan Y.; met30p, a yeast transcriptional inhibitor that responds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P39014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MT30_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas D., Kuras L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=X2180-1A;
MEDLINE-96069360; PubMed=8524217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MET30 OR YIL046W.
           EMBL; Z46861; CAA86905.1;
EMBL; L26505; AAA96717.1;
SGD; S0001308; MET30.
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 RFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRT
                                                                                                                                                                                                PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMGLEPNAAYSQSSAFGTSFDNGRAAPPRYMVTSALDSTIRLWETTTGRCLRTFFGHLEG
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                                                                                                                                                                  It is produced through
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                                                                                        (See http://www.isb-sib.ch/announce/
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InterPro;

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RESULT 9
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Best Local :
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DOMAIN 181 227
REPEAT 300 328
REPEAT 340 368
REPEAT 380 408
REPEAT 419 449
REPEAT 461 499
REPEAT 509 538
REPEAT 550 578
REPEAT 607 635
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                                                                                                                                                                                       466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 6.
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Pfam; PF00400; wD40; 7
Pfam; PF00646; F-box;
                                                                                                                                                            449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 NSNDKIRKL------ILDGILSTSCFPQLSYISSLVTHMIKIDFISILP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 IPEKNSLRQTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS 91
                                                                   -----KCMHTF---NGR--RLQRETQHTQTQSLGDKV
                                                                                              RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                        LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                               VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                   -----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                KRGIACLQYRD--RLVVSGSS-----
                                                                                                                                                                                                                                       ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
                                                                                                                                                                                                                                                                  ASPTDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH---
                                                                                                                                                                                                                                                                                              FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV
                                                                                                                                                                                                                                                                                                                         YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                                                                                    --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY 349
                                                                                                                                                                                                                                                                                                                                                                                 RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                            PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       ~--GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QELSLKILSYLDCQSLCNATRYCRKWQKLADDDRVWYHMCEQHI------DRKC
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD 2.
WD 3.
449 WD 4.
499 WD 5.
'9 WD 6.
WD 8 (POTENTIAL).
M -> I (IN REF. I).
5135D4BCAZELEB97 C.
'9 545; DP
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72835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Mismatches 202;
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD repeat.
650 AA
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                                                                     609
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PROSITE; PS00678; WD_REPEATS_1; 2.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
REPEAT
           209
                                                             223
                                                                                                                 155
                                                                                                                                                                                                                                                            117 VEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELYC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINBRPT
ProDom; PD000018; WD40; 4.
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Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U17251; AAA68968.1; -. InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a protein with beta-transducin repeats.";
Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995);
-!- FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTUDAL GENE EXPRESSION.
-!- INDUCTION: EXPRESSED ONLY UNDER LOW-SULFUR COUDITIONS.
-!- SIMILARITY: CONTAINS 8 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
                                                                                                                                                                      177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ranscription [
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfur controller-2 (SCON2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumar A., Paietta J.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95241499; PubMed=7724564;
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QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA
                                                             DGNA---
                                                                                                 QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP
                                                                                                                                                        KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS
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292 320
332 360
372 400
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                                                                                                                                                                                                                                                                                                                                          17.5%; Score 531.5; DB 1; Length 650; 25.0%; Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  72189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WD40
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RESULT 10
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Pfam; PF00646; F-box; 1.
Pfam; PF00320; GPROTEINBRPT.
PRODOm; PD00001B; WD40; 5.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SE10_CABEL STANDARD; PRT; 579 AA 093794; 15-JUL-1998 (Rel. 36, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat sel-10 protein
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J.M.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 F-BOX DOWAIN.
-!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sel-10 protein.
SEL-10 OR F55B12.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sims M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1996)
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                                                                                                                                                                          InterPro; IPR001680;
                                                                                                                                                                                                 InterPro; IPR001810; F-box.
                                                                                                                                                                                                                               EMBL; 279757; CAB02129.1; -
WormPep; F55B12.3; CE16120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
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RESULT 11
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PROSITE;
PROSITE;
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P53699;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
STRAIN-SGY126
Shieh J.C., W
                                         Saccharomycetales;
NCBI_TaxID=5476;
                                                               Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
                                                                                                 Cell division control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                            CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                               EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD
                                                                                                                                                                                                                                     AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD
                                                                                                                                                                                                                                                           TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI---
                                                                                                                                                                                                                                                                                 NTIRLWDI----ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP
                                                                                                                                                                                                                                                                                                        AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD 431
                                                                                                                                                                                                                                                                                                                              AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD
                                                                                                                                                                                                                                                                                                                                                  {\tt WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA}
                                                                                                                                                                                                                                                                                                                                                                        WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA
                                                                                                                                                                                                                                                                                                                                                                                                QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV
                                                                                                                                                                                                                                                                                                                                                                                                                    QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPV----ELGMKILHNLTGYDLLKVAQV
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PS00678;
PS50082;
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                                                                                                                                                         STANDARD;
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A.M.,
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28.8%;
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Pred. No. 1
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WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
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                                                                                                                                                         PRT;
                                                      Saccharomycotina;
Saccharomycetales;
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                                                                                                            update)
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                                                               Saccharomycetes;
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Matches
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Best Local
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SMART; SM00220; WD40; 7.

PROSITE; PS50181; FBOX; 1.

PROSITE; PS500678; WD_REPEATS_1; 4.

PROSITE; PS50082; WD_REPEATS_2; 4.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

Cell division; Mitosis; Sporulation; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
REPLICATION AND SEPARATION OF THE SPINILLE POLE BODIES TO FORM
POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTA1-HTB1 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001810;
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SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
GHLDRVYSTAIDFHSKTCFSGSMDSNINVWNFETGELKKVLVGHASLVGLLDLVDDVLVS
                                                                                             YIETFEGEFDNPYLIAVLSGHTQSVRSISGYGNIIISGSYDSTVRVWDLLDDGHCTHVLQ 518
                                                                                                                                                                                                                                        NTLIHH-----CEAVLHL----RFNNG------MMVTCSKDRSIAVWDM------ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                ---GNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCAAELVCKEWYRVTSDGMLWKKLIER--MVRTDSLWRGLAERRGWGQYLFKNKPPD---
                                             GH--RAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVS 445
                                                                                                                                                                                          HIFRGHTSTIRCLDIIHPAVIGKNQDGEDIVFPEYPLLITGSRDHNIHVWKLPVVDDSQD 458
                                                                                                                                                                                                                                                                                        VTGVDDKCISIYSTQTGQLMKVLEGHEGGVWALKYTGNTLVTGSTDRTVRVWNMKTGQCT 398
                                                                                                                                                                                                                                                                                                                                     VSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEML 340
                                                                                                                                                                                                                                                                                                                                                                                     REWSTLPEINSAQVLYKK----RKIIVNRWMDPKFKPHRISVSGHGNKVVTCLQHDDEKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00400; WD40; 7. PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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478
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351
391
431
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WD 2.
WD 3.
WD 4 (POTENTIAL).
WD 5.
WD 6.
WD 7.
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                                                                                                                                                -ASPIDITLR---
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Matches 164;

Conservative

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     Query Match
Best Local
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00320; WD40; 10.

PROSITE; PS5083; NACHT; 1.

PROSITE; PS00078; WD_REPEATS_1; 10.

PROSITE; PS50082; WD_REPEATS_2; 10.

PROSITE; PS50294; WD_REPEATS_REGION;

GTD_PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta homologous domain.";
Gene 162:135-139(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L28125; AAA85775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetatible incompatibility protein HET-E-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q00808;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pe
Sordariales; Lasiosphaeriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96009891; PubMed=7557402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS). SIMILARITY: CONTAINS 1 NACHT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED
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       Similarity
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307
869
911
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1037
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  15.0%;
26.0%;
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                                                                             149765
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GTP (1
WD 1.
WD 2.
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WD 5
WD 6
WD 6
WD 7
WD 7
WD 7
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Score 455.5; DB 1; Pred. No. 2.3e-26;
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                                                                           965FB319844E0651 CRC64;
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                       Length 1356;
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POP1_SCHPO STANDARD; PRT; 775 AA P87060; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1090
                                                                   "Fission yeast WD-repeat protein popl regulates genome ploidy through ubiquitin proteasome-mediated degradation of the CDK inhibitor Ruml and the S-phase initiator Cdc18."; Genes Dev. 11:1548-1560(1997).
                                                                                                                                                                                                                                                                                                                            WD-repeat protein popl. POP1 OR SPBC2G2.18.
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                                                                                                                                                                MEDLINE-97347242;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE=21848401; PubMed=11859360;
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                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRFN-NGMMVTC-SKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDF---DDKYIVSASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQRVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGHEELVRCIRF -- DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGHGDSVWSVAFSPDGQRVASGSIDGTIKIWD------AASGT-CTQTLEGHGGWVHS
                                                                                                                                                              PubMed=9203581;
                                                                                                                                                                                                                                                                                         Schizosaccharomycetes;
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   STRAIN-972;
MEDLINE-99144318; PubMed-9990507;
KOMINAMI K.-I., Ochotorena I., Toda T.;
Kominami K.-I., Ochotorena I., Toda T.;
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stongouros J., Peat N., Hayles J., Baker S., Basham D., Bowman Brooks K., Brown D., Brown S., Chillingworth T., Churcher C
                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complexes together with cullin-1 in fission
F-box) ubiquitin ligase.";
                                  REPEAT
REPEAT
                                                                       Repeat;
                                                                                                  PROSITE; PS50181; FBOX; 1.

PROSITE; PS00678; WD_REPEATS_1; 3.

PROSITE; PS50082; WD_REPEATS_2; 4.

PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                             EMBL; AL022103; CAA17898.1;
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes Cells 3:721-735(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Involved
                                                                                                                                                                                 SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                    PRINTS; PR00320; GPROTEINBRPT PRODOM; PD000018; WD40; 3.
                   REPEAT
                                                                                                                                                                                                                                                            Piam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Homodimer and heterodimer with pop2. Binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are subsequently ubiquitinated and targeted to the for degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Involved in maintenance of ploidy through proteasome dependent degradation of CDK inhibitor ruml and S-phase initiator cdc18. Functions as a recognition factor for ruml and cdc18, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cdc18
                                                                                                                                                                                                                                                          PF00400; WD40; 7
PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                   Y08391; CAA69671.1; -.
repeat.
298
444
484
575
615
 345
472
538
603
   F-BOX
WD 1.
WD 2.
WD 3.
WD 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26S proteasome
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RESULT 14
CC4-Y24-Y
ID CC4-Y2
ID CC4-Y2
AC P078-Y
AC P07
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                                                                                                                                                                                                                                                                                                                                                             CC4_YEAST STANDARD; PRT; P07834; 01-AUG-1988 (Rel. 08, Created) 01-NOV-1995 (Rel. 32, Last sequence 15-JUN-2002 (Rel. 41, Last annotat Cell division control protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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J. Mol.
[2]
                                                         a related pseudogene.
                                                                                                                                                                                                                                                                                                                                                 CDC4 OR YFL009W.
                                                                                                                                          MEDLINE=88011240; PubMed=3309335;
                                                                                                                                                                                                                                                                                     Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
SEQUENCE
                                                                        "Structural comparison of the yeast
                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                          Saccharomycetales;
                                                                                                            Cochem J., Byers B.
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TSTCEFVRTLNGHK----RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC
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                        Biol. 195:233-245(1987).
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                                                                                                                                                                                                                                                                                  Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                          Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687
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25.8%;
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Pred. No. 1.7e-26;
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                                                                                                                                                                                                                                                                                  Saccharomycetes;
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PROSITE; PS50082; WD_REPEATS_2; 5.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00320; GPROTEINBRPT
ProDom; PD000018; WD40; 4.
SMART; SM00256; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage by and for one and its requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00256; FBOX; SMART; SM00320; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D50617; BAA09229.1;
EMBL; Z46255; CAA86341.1;
PIR; A26867; A26867.
SGD; S0001885; CDC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288c / AB972;
Barrell B.G., Churcher C.,
Submitted (SEP-1994) to th
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Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama
Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
Saccharomyces cerevisiae.";
169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00400; WD40; Pfam; PF00646; F-box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001810;
InterPro; IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X05625; CAA29113.1; -.
                                                                245
                                                                                                                    109
                                                                                                                                                         194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288c / AB972;
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                                                                                                                                                                                                          56 TYCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK------ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTION ACTIVATION.
SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FOR POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTAL-HTB1 LOCUS
                                                     -----NLLFRLYANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED
                                                                                                      SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division
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                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                            779 AA;
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitosis;
2 319
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449
493
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                                                                                                                                                                                                                                                                   ; 08
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                                                                                                                                                                                                                                                                                Score 399; Db ...
No. 2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                       WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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MEDLINE=21848401; PubMed=11859360;
MCOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Hukke E.J., Hunt S., Jagels K.,
Holroyd S., Hornsby T., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                 MEDLINE-98318628; PubMed-9653157;
Jallepalli P.V., Tien D., Kelly T.J.;
"sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml proteins for degradation and stops unwanted diploidization in fission
                                                                                                                                                                                                                                                                                                                 MEDLINE-99227353; PubMed-10209119; Wolf D.A., McKeon F., Jackson P.K.; "F-box/WD-repeat proteins poplp and Sudlp/Pop2p form complexes that bind and direct the proteolysis of cdc18p."; Curr. Biol. 9:373-376(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccuarum, — .

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WD-repeat protein pop2 (Proteolysis factor POP2 OR SUD1 OR SPAC4D7.03. Schizosaccharomyces pombe (Fission yeast).
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                                                                                                                                                                                                          yeast
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                                                                                                                                                                                           Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                         U.S.A.
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Query Match Best Local :

Similarity

Score Pred.

396.5; D

DB 1;

Length 703;

SEQUENCE

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79605 MW; 13.1%; 23.3%;

0336A0568C152396 CRC64;

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Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G. Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kominami K.-I., Ochotorena I., Toda T.,
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero-and homo-
complexes together with cullin-1 in fission yeast SCF (Skip-cullin-1-
F-box) ubiquitin ligase.";
Genes Cells: 3:721-735(1998).

Genes Cells: 3:721-735(1998).

-!- FUNCTION: Involved in maintenance of ploidy through proteasome
dependent degradation of CDK inhibitor ruml and S-phase initiator
cdcl8. Functions as a recognition factor for ruml and cdcl8, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Berk M., Lehrach H., Reinhardt R., Pohl T.M.,
                                                   REPEAT
REPEAT
                                                                                                                      Repeat;
                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                EMBL: Z98602; CAB11275.1; -. Interpro; IPR001810; F-box. Interpro; IPR001680; WD40. Pfam; PF00440; WD40; 7. Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                           PRINTS; PR00320; GPROTEINBRPT PRODOM: PD000018; WD40; 3. SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer and heterodimer with popl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for degradation.
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PS50082;
PS50294;
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                               ) repeat.
236
389
429
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545
587
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                                                                                                                                                                         WD_REPEATS_1; 3. WD_REPEATS_2; 6.
                                                                                                                                                         WD_REPEATS_REGION;
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WD 2.
WD 3.
WD 4.
WD 5.
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Maten	
Ωy	14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCL 59
Db S	96 KENESTENVSYKCLDHSPPDSVPGDFSISLVPQRNFL-YSHSSLPPKIISIDRNNRIKLD 154
ОУ	60 ASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEK-EKELCVKYFEQWSESDQVEFVE 118
Db 15	155 NSISSNSDNFPPSPKVDTSNTVSPGSKPISEDLEDLNLQSIVQTFEDLPEGIQ-SYAF 211
Qу 11	119 HLISQMCHYQHGH-INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 177
Db 21	212 FQLLRSCNRQSMRLLLNECEPLLKKDILSNLPFSIVQSILLNLDIHSFLSCRLVSP 267
Qy 17	178 EWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPN 229
Db 26	268 TWNRILDVHTSYWKHMFSLFGFQINENDWKYANPNLNRPPFLHND 312
Qy 23	230 SFYRALYPKIIQDIETIESNWRCGRHSLQR 259
Db 31	313 QISDDYFPEIFKRHFLNRKRWLFPSIPPSHLSFPIHVPNFMITSLLLH 360
Оу 26	260IHCRSETSK-GVYCLQYDDQKIVSGLRDNTIKIWDKNT 296
Db 36	361 KDRIITTSGSGTIQIHNAITGVLEARLEGHKEGVWAVKIHENTLVSGSIDKTVRVWNIEK 420
Оу 29	297 LECKRILTGHTGSVLCLQY
Db 43	421 AKCTHIFRGHISIIRCLEILVPSRLIRHGVEIVEPDQPYIVSGSRDHTLRVW 472
Οу 34	341 NTLIHHCEAVLHLRENNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDD 400
Db 47	473KLPKNTDPPYLPDNTNSIDRWE-KNPYFVHTLIGHTDSVRTISGYG 517
Оу 40	401 KYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIE 458
Db 51	518 DILVSGSYDSSIRIWRVSTGECLYHLRGHSLRIYSVLYEPERNICISGSMDKSIRVWDLS 577
ОУ 45	459 CGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH 518
Db 57	578 TGTCKYVLEGHDAFVTLLNVFQNRLISGSADSTIRIWDLNTGKPLMVLPSN 628
Оу 51	519 SGRVFRLQFDEFQIVSSSHDDTILIWD 545
Db 62	629 SGYISSFVSDEHKII-SGNDGSVKLWD 654

Search completed: February 20, 2003, 09:54:19 Job time : 19 secs

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Maximum Match 100%
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Maximum DB seq length: 200000000
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re greater than or equal to the score of the result being printed,
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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Match Length
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-09-172-841-2
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9999 7, CAN CAN CAN OF		Match Local Similarity es 125; Conserva	ESULT 1 S-09-172-841-2 Sequence 2, Application US/0 Patent NO. 6232081 GENERAL INFORMATION: APPLICANT: Harper, Jeffrey APPLICANT: Elledge, Stephen TITLE OF INVENTION: F-BOX P FILE REFERENCE: BCM-03510 CURRENT FILING DATE: 1998-1 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-1 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 126 TYPE: DNA ORGANISM: Homo sapiens S-09-172-841-2			35.4 34.8 34.6
N H H A TH D H O C	GCTCGGG CTCGGG GCTGCTG TGTGCTG TGTGCTG	ilarity Conser	41-2 2, Application US/09172841 2, Application US/09172841 1, 6233081 INFORMATION: TT: Elledge, Jeffrey W. TT: Elledge, Stephen J. INVENTION: F-BOX PROTEINS ERENCE: BCM-03510 APPLICATION UNMBER: US/09/ FILING DATE: 1998-10-15 APPLICATION NUMBER: 08/951 FILING DATE: 1997-10-16			
on Wil Wil Ka	GATTGG/ GATTGG/ GTGAACT CTGAACT	5.8 99.2 vative	: Jeffrey W. Stephen F-BOX phen M-03510 M-0351		2144 22446 22246 22246 22246 22246 25546 5558 3747 7042 7042 7042 7042	12286 3465 1611 1848
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US/08914999 Alexey G. liam N. ren S. ELONGATION FACTOR-2 KINASE (EF- AND METHODS OF USE THEREFOR 25 S:	CTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAA	Score 124.4; DB 4; Pred. No. 6.2e-31; 0; Mismatches 1;	Al. (17)	ALIGNMENTS	US-U8-767-993-10 US-09-032-742-21 US-09-032-742-22 US-09-032-742-25 US-09-032-742-25 US-09-032-742-25 US-09-032-742-25 US-09-032-742-25 US-09-032-742-25 US-09-032-742-25 US-09-032-508-1 US-09-09-508-11 US-09-09-354-21 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1 US-09-098-310-1	US-09-357-206A-1 US-08-914-999-5 US-09-302-769-13 US-08-313-553-10
E-2 KINASE)	TACCTGGATGCCAAA 570	Length 126; Indels 0; Gaps			Sequence 10, Appl Sequence 3, Appl Sequence 21, Appl Sequence 22, Appl Sequence 24, Appl Sequence 25, Appl Sequence 103, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli	1, 13
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INFORMATION FOR SEQ ID NO: 7:
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                   1439 TAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTC 1498
                                                                   1901 GTATATTAGGTACCAATCTCTACAGTGGCTCCTATGATAAAACTATAAGAGTTTGGAATT 1960
                                                                                                                                                                                                        1319 CAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGC 1378
                                                                                                                                                                                                                                                                                1259 ACTITGATGACAAGTACAITGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACA 1318
                                                                                                                                                                                                                                                                                                                                               1730 TGGAATGTAAATATACCCTTGAAAGTCATGCCAGA------GCCGTCAAAACACTTT 1780
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ORIGINAL SOURCE:
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LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                      1781 GTATATCTGGTCAATATTTATTTAGTGGTTCAAATGATAAAACTATCAAGGTTTGGGATT 1840
                                                                                                                                                                                                                                                                                                                                                                                           1199 CAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                      1670 ATAAATATTTGTTTAGTGGTTCCTCTGACAAAACTATCAAAGTTTGGGATTTGAAAACTT 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1139 ATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCC 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1610 TAAGATGTATTTTACTTTGGAGGGTCATGATAAACCTGTCCATACGGTTCTATTGAATG 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1079 GTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATA 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1019 AGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1490 TGGAATGTGTTCAAACCTTGAAAGGTCATGAAGGTCCAGTTGAATCAATTTGTTATAATG 1549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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STREET: 41
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                                                                                                               AGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
                                                                                                                                                               TGAAAACTTTTCGTTGTAACTACACTCTAAAAGGTCATACTAAAATGGGTCACCACTATCT 1900
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    Mismatches

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                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
1453 IGITTACGAGIGTTAGAAGGCCATGAGGAATTGGTGCGTIGTATTCGATTTGATAACAAG 1512
                                                              1138 ATACTTGTCACTGGATCACGAGATACCACTCTTCGTGTATGGGACGTAGAATCCGGACGT 1197
                                                                                                                                                                                                                      1018 TATATTGTTAGCGGGTCCACTGATAGAACTGTAAAAGTTTGGAGTACTGTAGATGGTTCA 1077
                                                                                                                                                                                                                                                           1273 TACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAA 1332
                                                                                                 1393 CTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCA 1452
                                                                                                                                         1078 CTTCTTCATACACTTCAAGGACATACTTCCACTGTTCGATGCCATGGCTATGGCTGGTTCC 1137
                                                                                                                                                                                1333 TTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGACAGG 1392
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                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Greenwald, APPLICANT: Hubbard, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2081 TAG 2083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2021 TAATTTGTGATAAATTATTTATTTACTGCTAGTGACGATAATACAATTAAAATTTGGGATT 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1499 GATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATC 1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 24-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                       162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2481 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                       Conservative
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91..1854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278-0525
                                                                                                                                                                                                                                                                                                                       3.1%; Score 67.2; DB 3; Length 2481; 50.6%; Pred. No. 2.6e-11;
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US-08-283-917-8
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US-08-283-917-8
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                                                                                                         Query Match
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5849557
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: 03-AUG-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
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1184 TCATTTTCCATCCTGTGTTCAGTGTTATGGTCTCTGCTTCAGAGGATGCTACAATTAAGG 1243
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                     1001 TCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAG 1060
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK ADDRESSEE: NEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP 209943/1993 FILING DATE: 03-AUG-1993
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                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                        Match 2.4%;
Local Similarity 47.3%;
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                                                                      262;
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ARAI, HIROYUKI
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                                                                        Conservative
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                                                                      Score 50.8; DB 2;
Pred. No. 5.6e-06;
0; Mismatches 277;
                                                                                                         Length 2085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 03-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OXIDIZED PHOPHOL THILE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                     APPLICATION NUMBER: JP 209943/1993
                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington STATE: Virginia
                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAN
ADDRESSEE: NEUSTADT, P.C.
                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGAACTATAAAAGGTATGGAACACAAGTACTTGTGAATTTTGTAAGGACCTTAAAATGGAC 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCACTTGCGTTTCAATAATGG------CATGATGGTGACCTGCTCCAAAGATCGTTCCA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGGGATTATGAGACTGGAGATTTTGAACGAACTCTTAAGGGGCCATACAGACTCTGTAC 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAG 1468
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                                                                                                                                                                                                                                                                                                                                22202
Oblon,
                                                                                                                                                                                                                                                                                                                                                                                                              1755 S. Jefferson Davis Highway, Suite 400
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TSUJIMOTO, MASAFUMI
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No.
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5880272man F
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REGISTRATION NUMBER:

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; LOCATION:
US-08-961-716-8
                                                             Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                       1721 TCTCTGAAGCAACA 1734
                                                                                                                                                                                                                                                                                                                                              1469 AAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGG 1528
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    APPLICANT:
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REFERENCE/DOCKET NUMBER: 2292-030-0
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
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                      DORNER, F. SCHEIFLINGER, F.
FALKNER, F. G.
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Best Local :
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1088 RRRRRRRRRRRRRRRRRRRRRRRTCGCAAGCTCCCTCGACCTGCAG 1043
                                                                                                                                      REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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APPLICATION STATE 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                               946 GATAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAG 991
                                                                                                                                                                                                                                             766 AGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGT 825
                                                                                                                                                                                                                                                                                                                                                                                      646 ATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGG 705
                                                                                                                                                                                                                                                                                                                    706 GGACAGTATTTATTCAAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTAT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 GAACTTGTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTT 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     TTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGG 945
                                                                                                                                                                          GGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative 218; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 2.3%; Score 50; DB 1; Length 7218; Similarity 4.9%; Pred. No. 2.4e-05;
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Hest Local Similarity 52.6%;
Matches 131; Conservation
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
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LENGTH: 2152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                   1265 ATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTA 1324
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1805 TTGGACATGGTTTGATGGTTGGAGAATTAAAAGGCCACACTGATACAGTCTGTTCACTTA 1864
                                    1439 TAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCCATGAGGAATTGGTGCGTTGTATTC 1498
                                                                               1745 CTCCCAATGGGAGATTCCTGGCTACAGGAGCAACAGATGGCAGAGTGCTTCTTTGGGATA 1804
                                                                                                                                                               1325 CTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTA-- 1382
                                                                                                                                                                                                                                             1625 ATTCTAATTATGTTGCTACGGGCTCTGCAGACAGAACTGTGCGGCTCTGGGGACGTCCTGA 1684
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                                                                                                                      1383 ----CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Osman, Richard A REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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Tanese, Naoko
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                                                                                                                                                                                                                                                                                                                                                  Score 47.8; DB 1; Pred. No. 5.5e-05;
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                                                                                                                                                                                                                                                                                                                                           TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 harr
Type
                                                                                                                                                              Matches 131;
                                                                                                                                                                             Query Match 2.2%;
Best Local Similarity 52.6%;
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                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE NUMBER OF SEQUENCES: 36
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TELECOMMUNICATION INFORMATION:
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1383 ----CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACA 1438
                                1325 CTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTA-- 1382
                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                              NAME/KEY:
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(415) 39
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Tanese, Naoko
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Comai, Lucio
                                                                                                                                                            Conservative
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Weinzierl, Robert O.J.
VENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS
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09-MAY-1996
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Pred. No. 5.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 30472/114
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INFORMATION FOR SEQ ID NO: 14:
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TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC COMPONS NO SYSTEM: PC-DOS/MS-DOS
1774 AGATAAATAACCATACACTGACCTCATACTTGCCCCAGGACCCCATTAAAGTTGCCGGTATTT 1833
                                                                         1714 GATCCAGCTGCCCAAGCTGAACCCCCCCCCTTCCCCCTTCTCGAACATACACCTACATCTCC 1773
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                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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CURRENT APPLICATION DATA:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
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                                                                                                                                                                                                                                                    CLONE:
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                                                                                                                                                                        ocal Similarity
                                                                                                                                                                                                                                                                                                                                           LENGTH:
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                       Conservative 210;
                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                    1.9%; Score 39.8; DB 3.6%; Pred. No. 0.052;
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                                                                                                                                                     Mismatches
                                                                                                                                                                                      DB 1; Length 7218;
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US-08-664-596B-1
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US-08-664-596B-1
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                                                                                                                                                        TELEPAX: (61/)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
Best Local Similarity 51.4%;
Matches 89; Conservative
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                                                                                                                                                                                                                                               NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                         TOPOLOGY:
                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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LaVallie, Edward
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                                                                                                                                        double
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                Score 38.6; DB 1; Length 433; Pred. No. 0.019; 0; Mismatches 84; Indels
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227 CTATATTCTGCATCGTGGGACTCTACAGTGAAGGTGTGGTGTCTGGTGTTCCTGC

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Best Local Similarity
                                                                                                                                                                                                    Matches
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1516 ATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGGATCTTGTGGCTGC 1568
                                                                                                                                                             1396 GTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGT 1455
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1516 ATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGC 1568
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                                                                                       1456 TTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGG 1515
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                                                        167 CAGGACACGTTAATGGGACATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/738,367
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                                                                                                                            GTCATAACTTCTTCATGGGATAATAATGTCTATTTTTATTCCATAGCATTTGGAAGACGC 166
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Merberg, David
Treacy, Maurice
Spaulding, Vikki
Spaulding, Vikki
AND POLYNUCLEOTIDES
TOTAL THEM
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McCoy, John
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                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                             Score 38.6; DB 1,
Pred. No. 0.019;
"" matches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                 DB 1; Length 433;
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US-08-738-367-6
                               RESULT 13
US-09-156-425-1
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Sequence 1, Application US/09156425B Patent No. 5962671
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                                                                                                                                                                                                                                                     1396 GTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGT 1455
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Genetics
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CTTY: Cambridge
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                                                                                                                                                                                                                                                                                Local 89;
                                                                                               227 CTATATTCTGCATCGTGGGACTCTACAGTGAAGGTGTGGTCTGGTGTTCCTGC 279
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                            CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAACAGG
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                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                   733 base pairs
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VENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
VENTION: ENCODING THEM
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Treacy, Maurice
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GENERAL INFORMATION:

APPLICANT: Baker, Brenda F APPLICANT: Cowsert, Lex M.

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; LOCATION: (18)..(1265)
US-08-965-048-3
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; LOCATION: (13)..(2766)
US-09-156-425-1
US-09-318-448-11
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US-08-965-048-3/c
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                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.7%;
Best Local Similarity 56.1%;
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LENGTH: 3380
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APPLICANT: Freimer, Welson
APPLICANT: Freimer, Welson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERENCE: 7853-093
CURRENT EPPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
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SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                             1422 TAA 1420
                                                                                                                                                                                  1482 ATCTAAACTTATTTAAGGATTAAGTAGGATAACGTGCATTGATTTGCTAAAAGAATCAAG 1423
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                                                                                                                                      870 CAA 872
                                                                                                                                                                                                                            810 ATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAG 869
                                                                                                                                                                                                                                                                                                                      750 TCCCAACTCTTTTTATAGAGCACTTTATCCTAAAATTATACAAGACATTGAGACAATAGA 809
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                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Sequence 11, Application US/09318448

Patent No. 6210950

GENERAL INFORMATION:
APPLICANT: Senroos, Feward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 MDPAEAVLQEKALKEMNSSE......PAAQAEPPRSPSRTYTYISR 569
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 GenCore version 5.1.3 Compugen Ltd.
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T16607
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T43557
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T46660
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43 GTSSMIVPKQRKLSANYEKEKELCVKYFEQWS: 138 PMLQRDFITALPARGLDHIAENILSYLDAKSIC	re 2597; DB 2; Length 518; d: No. 1.2e-193; Mismatches 8; Indels 30; Gap MSCARLCLNQETVCLASTAMKTENCVAKTKLAN 7TKLAN 7 FEGWSESDQVEFVEHLISQMCHYOHGHINSYLK 1	~	30 330 10.9 333 2 GB5034 probable WD-repeat 31 320 10.5 934 2 AG1889 WD-40 repeat prote 32 318.5 10.3 376 2 T19266 hypothetical prote 34 312.5 10.3 376 2 T29266 hypothetical prote 35 312 10.3 876 2 T51507 WD-40 repeat prote 36 312 10.3 876 2 T51507 WD-40 repeat protei 37 307.5 10.1 1693 2 S76086 WD-40 repeat protei 39 306.5 10.1 598 2 AB28415 WD-repeat protein 40 305 10.1 189 2 AH2154 WD-repeat protein 41 299.5 9.9 1194 2 S33263 WD-repeat protein 42 298.5 9.8 357 2 AF1890 WD-repeat protein 43 297.5 9.8 357 2 AF1890 WD-repeat protein 44 297.5 9.8 357 2 AF1890 WD-repeat protein 45 296.5 9.8 304 2 AG1837 WD-40 repeat protein 45 296.5 9.8 304 2 AG1837 WD-40 repeat protein 45 296.5 9.8 304 2 AG1837 WD-40 repeat protein 45 296.5 9.8 304 2 AG1837 WD-40 repeat protein 45 296.5 9.8 304 2 AG1837
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A;Accession: T16607
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A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-701 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K10B2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 LKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 VAALDPRAPAGTICLRTIVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 SMIVPKQR-----KLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 RKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN-------GTS
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                                                                       SHDDTILIWDFLNDPAAQAEPPRSPSRT 563
                                                                                                          IRFDEKRIVSGAYDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSS
                                                                                                                                     IREDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                                                                            SMDTLEFYRTLAGHRRGIACLQYRGRLVVSGSSDNTIRLWDIHSGVCLRVLEGHEELVRC
                                                                                                                                                                                                                                    NTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC 475
                                                                                                                                                                                                                                                                              ANGIMYTCSKDRSIAVWDMYSPRDITIRRYLYGHRAAVNVYDFDDRYIVSASGDRTIKVW
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                                                                                                                                                                                                                                                                                                                                                              DYSCSRILSGHTGSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRF 346
                                                                                                                                                                                                                                                                                                                                                                                    TLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRF 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                YPKIIRDIHNIDNNWKRGNYKMTRINCQSENSKGVYCLQYDDDKIVSGLRDNTIKIWDRK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFLFPSRNTQIFLSYSRSFSSFSEVL----KWSEHEQLDFMDKIVHRLSHYQLGKVDNF 110
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9; Mismatches 116; Indels
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           R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1997
A;Reference number: 221818
                                                                                        probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
A; Reference number: A; Accession: T38932
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C:Superfamily: unassigned WD repeat proteins; WD repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;MCDOugall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; submitted to the EMBL Data Library, January 2000 A;Reference number: Z25046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SPAC29E6.01; SPDB:SPAC30.05
A;Map position: 1
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A;Experimental source: strain 972h(-); cosmid c30
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A; Residues: 1-506 <MCD>
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                                                                            456
                                                                                                              498 VAALDPRAPAGTLCLRTLVEH------SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 TSDGMLWKKLI------ERMVRTDSLWRG------LAERRGWG------
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                                                                                                                                                                                                                                                              ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF
                                                                                                                                                                YNGKFIVSGSSDLTIRIFEASSGKLLRMLQGHEDLIRTVRFNDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                             YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                                ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                                                                                                                                                                                                                                                                                SGSSDSTITIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163;
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                                                                 ----FNTGEQHCVLHNSRNSRVFGLQFDHRRIIACTHSSEILVWNF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.7%; Score 690; DB 2; 30.4%; Pred. No. 1.3e-45;
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T38932

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-605 <BAD>
A;Residues: 1-605 <BAD>
A;Cross-references: EMBL:204864; PIDN:CAB08168.1; GSPDB:GN00066; SPDB:SPAC57A10.05c
A;Experimental source: strain 972h-; cosmid c57A10
C;Genetics:
                                                                                                                        A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-640 <ODE>
A;Residues: 1-640 <ODE>
A;Cross-references: GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763300; MIPS:YIL046w
R;Thomas, D.; Cherest, H.; Barbey, R.; Surdin-Kerjan, Y.
submitted to the EMBL Data Library, December 1993
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A;Map position: 1
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
A;Cross-references: EMBL:L26505; NID:g432493; PID:g432494 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                      C; Species: Saccharomyces cerevisiae
C; Date: 28-May-1993 #sequence_revision
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                                       A; Molecule type: DNA
A; Residues: 1-60, 'I', 62-640 <THO>
                                                                                   A; Reference number: $43750
A; Accession: $43750
                                                                                                                                                                                                                                            A; Reference number: S49931
A; Accession: S49932
                                                                                                                                                                                                                                                                                                          C; Accession: S49932; S43750 R; Odell, C.; Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                             MET30 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YI9905.02; protein YIL046w
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                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASPIDITLRRVLVGHRAAVNVVDF - - DDKYIVSASGDRTIKVWNISTCEFVRILNGHKRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGKRITLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTFSAHIGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
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C;Superfamily: unassigned WD repeat proteins;
F;298-329/Domain: WD repeat homology <WDl>
F;338-369/Domain: WD repeat homology <WD2>
                                                                                                                                      R;Kumar, A.; Paietta, J.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
A;Title: The sulfur controller-2 negative regulate
A;Reference number: Z23121; MUID:95241499; PMID:77
A;Accession: T46660
                                                                                                                                                                                                                                           C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000
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A; Map position:
A; Introns: 75/3;
                                                                                    A; Molecule type: DNA
A; Residues: 1-650 < KUM>
                                                                                                                                                                                                                               C; Accession: T46660
                                                                                                                                                                                                                                                                              sulfur controller-2 protein [imported] - Neurospora crassa
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                                 A;Gene: scon-2
                                                                    A;Cross-references: EMBL:U17251;
                                                                                                                     A;Status: preliminary;
                                                   Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GWGQYLFKNK------PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRGIACLQYRD--RLVVSGSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM
                                                                                                                                                                                                                                                                                                                                                                                                          RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESRTCYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASPIDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- QELSLKILSYLDCQSLCNATRYCRKWQKLADDDRVWYHMCEQHI--
                                                                                                                                                                                                                                                                                                                                                                                                                                           LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167;
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319/1;
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 354/1
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28.9%;
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                                                                  NID:g806757; PIDN:AAA68968.1; PID:g806758
                                                                                                                                                                         negative regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 545; DB 2;
Pred. No. 3.2e-34;
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                                                                                                                       GB/EMBL/DDBJ
                                                                                                                                                          PMID:7724564
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C;Function:
A;Description: negatively regulates sulfur structural gene expression
A;Description: negatively regulates sulfur structural gene expression
A;Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to the
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                 submitted to the RMBL Data Library, September 1996
A;Reference number: Z19602
A;Accession: T22703
                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F55B12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22703
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                                                                                                        A; Map position:
A; Introns: 22/3;
                                                                                                                                                          A;Gene:
                                                                                                                                                                                                         A;Cross-references: EMBL:Z79757; PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3 A;Experimental source: clone F55B12
                                                                                                                                                                                                                                                          A; Residues: 1-579 <WIL>
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                          R;Sims,
          Matches
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 MSHAQIERAGSPGSHSSSHNLLPSSLPSGDEDVRHLYGSAFVADESRPLPPRYFMTGGLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 VY----RDRWQVSYNWKNSRYKLSVL---KGHENGVTCLQLDDNILATGSYDTTIKIWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 LYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 QRWRTLADSDAVWVRMCEQHVNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 LQGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAQKVLCYLDTVSLTKAAQVS 154
                                 Local
                                                                                                                                                          CESP: F55B12.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDF 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRTI 412
          150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLWDLDTRQVIRTYEGHVGHVQQVLILPPEYEPDEEVLNGASQDNQDAMSVSSGGSGSPS
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                                                                                                           22/3;
                            Similarity
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                                                                                             45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
17.1%; Score 520; DB 2; Length 579; 28.8%; Pred. No. 2.4e-32; tive 78; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.5%; Score 531.5; 25.0%; Pred. No. 3.6
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     70;
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  Gaps
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C;Superfamily: unassigned WD repeat proteins; WD
F;18-51,/Domain: WD repeat homology <WD1>
F;104-137/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces p C;Species: Schizosaccharomyces pombe C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000 C;Accession: T38502; 862507 R;Jones, L.; Murphy, L.; McNeil, A.; Simpson, I.; Harris, D.; Barrell, B.G.; Rajandre submitted to the EMBL Data Library, October 1995
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                                                                                                Db
                                                                                                                                                                                                   Вb
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A; Residues: 1-267 <J02>
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A; Accession: T38502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z66525; NID:g1044926; PIDN:CAA91423.1; PID:g1044927; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вþ
                                                                                                                                                                                                                                                                                                    Matches
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                                            402 --YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507
                                                                                                                                                                                                                                                286 DNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VIITGSSDSTVRVWDVNTGEMLNTL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI------H 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 NTIRLWDI---ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 AVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 WSTVDGSLLHTLQGHTSTVRCMAMAGSILVTGSRDTTLRVWDVESGRHLA---TLHGHHA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 QIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 CDLNVHRFLKLQKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 PN-SFYRALYPKIIQDI------ETIESNWRCGRHSLQRIHCRSETSKGVYCL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 CKEWYRVTSDGMLWKKL-IERMV-----RTDSLWRGLAERRGWGQYLFKNKPPDGNAP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 FVEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                             61 FGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAEACM-HVLRGHLASVNSVQYSSK 119
                                                                                                                                                                                                                                                                                                                         Local
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TGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQYNGKFIVSGSSDLTIRIFEASS 179
                                                                                                                                            IHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTDITLRRVLVGHRAAVNVVDFDDK 401
                                                                                                                                                                                              DRTVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLVSGSSDSTIIIWDWQNRRPLKVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD 86
                                                                                                                                                                                                                                                                                                    104;
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                    17.1%; Score 519.5; 38.0%; Pred. No. 8.
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C;Accession: T18521
R;Saupe, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
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C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γ
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A;Accession: T18521
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A; Residues: 1-1356 <SAU>
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Best Local :
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                                                                                                                         1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 LVFPTGIEDVSYIIFWRSLNVMSQKLRRDIYCLNAPGFLIDNVRVPDPDPLATVRYSCIY 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    581 EMPDDVSDDPESLEEIVKLCGSFLIIRERTVYFVHQSAKDFLLGTASDKASNKASQEAFE 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         760
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                                                                                                                                                                                                                          973 VAFSPDGQRVASGSGDKTIKIWDTASG---TCTQTLEGHGGSVWSVAFSPDGQRVASGSD 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 MIVPK-----QRKLSASYEKEKE--LCVKYFEQWSESDQVEFVEHL--ISQMCHY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 EPPRKIIPEKNSLRQTYNSCAR-LCLNQETVCLASTAMK----TENCVAKTKLANGTSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHGHINSYLKP-----MLQRD-----FIT------ALPARGLDHI--AEN 159
                                                                                                                                                                                                                                                                                                                                                                           NTLECKRILTGHTGSVLCLQY--DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLH 352
                                                                                                                                                                                                                                                                                                                                                                                                                              GORVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDA 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QRIHCRS-----ETSKG--------YYCLQY--DDQKIVSGLRDNTIKIWDK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKNKPPDGNAPPNSFYRALY----PKIIQDIETIESNWRCGRHSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER----MVRTDSLWRGLAERRGWGQYL 216
                                                                                                                                                                    DRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACLRVL 466
                                                                                                                                                                                                                                                                             LRFN-NGMMVTC-SKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDF--DDKYIVSASG 408
                                                                                                                                                                                                                                                                                                                             ASGTCTQTLEGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLS 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F-----APTDSMIKKIFKKEEPGWISTISVVEAEWNACTQTLEGHGSSVLSVAFSAD
                     EGHGDSVWSVAFSPDGQRVASGSIDGTIKIWD------AASGT-CTQTLEGHGGWVHS 1140
                                                                      EGHEELVRCIRF - - DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164; Conservative
                                                                                                                      DKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASGSDDHTIKIWDAVSGTCTQTL 1089
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A;Description: Fission yeast WD repeat protein Popl
A;Reference number: Z22925
A;Accession: T45136
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A;Experimental source: strain 972h-; cosmid c2G2
C;Genetics:
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A;Experimental source: strain h- 972
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kominami, K.; Toda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z21842
A; Accession: T40157
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A; Residues: 1-775 < KOM>
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A; Residues: 1-775 < WOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 LQF--DEFQIVSSSHDDTILIWDFLNDPAAQ 553
                             417
                                                                                                                                                                                                                                                                                                                                                                                         357 DSKIRTMCLEQSLSA----- 389
                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ERMYRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYR-VTSDGMLWKKL------I 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180
                                                                                                                                 371 VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN------
                                                                                                                                                                                 450 WTFEYVGDTLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTTDTD----
                                                                                                                                                                                                                                  311 LCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIA 370
                                                                                                                                                                                                                                                                                                                                      254 RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 QEKALKFMNSSEREDC------NNGEPPRKIIPEKNSLRQTY-NSCARLCLNQET 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTGFPA----EITNLVLTHLDAPSLCAVSQVSHHWYKLVSSNEELWKSLFLKDGFFWDSI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFQKNF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SYEKEKEL----CVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144
                                                                                                                                                                                                                                                                                     LHAPEKIKRCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                              -DYEKE-----NRPASNDANSMPPYIISSSRDCTIRLWSLPCLDDPPFVNVNE 552
---TSTCEFVRTLNGHK---RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 453; DB 2; 25.8%; Pred. No. 5.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LASTAMKTENCVAKTKLANGTSSMIVPKQRKLSA----- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 229; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pop1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 775;
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;MoLecule type: DNA
A;Residues: 1-1227 <br/>KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179<br/>A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
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                         503 PRAPAGTLCLRTLVEHSGRVFRLQF--DEFQIVSSSHDDTILIWDFL 547
                                                                          791 SSGEDSTVRLWDVKTGQCWQIFEGHSKKVYSVRFSPDGQTLASCGEDRSIKLWDIQRG-- 848
                                                                                                                                                                                                                                         393 VNVVDF----DDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYR--DRLVV 444
                                                                                                                                                                                                                                                                                             674 HTGECLKTLSKNTNKYYSVAFSPDGRILASASQDQTIKLWDIATG---NCQQTLIGHDDW 730
                                                                                                                                                                                                                                                                                                                                                                                                           614 GKYFATGLMNGEIRLWQTSDNKQLRIYKGHTAWVWAFAFSPDSRMLASGSADSTIKLWDV 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 KIPDESPIDLSGRDFSGLTIWQAYFKEVKLKETIFANSDLTGSVFTETMSSVVSVKFSPD 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPN--SFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 IIQDIETIESN------WRCGRHSL---QRIHCRS-----ETSKGVYCLQY--D 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              479 -----INTY--PLMK------ARSLDYI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELYCKEWY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 EKASSTQGEKEAESSKFGLESVVM---EYITAKFIENS-----LEEFSQTKKLDF---- 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 EKKVMYSLGANREYVSFRELKDDWLTTESPIKVMEALESLLR-----RSLIEKASPTLI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 LRVLEGHEELVRCIRFDNKR--IVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         553 NPDQNNDFTSATTNPFYIRTLRGHTDSYREVACL---GDLIVSASYDGTLRVWKASTGYC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 EKALKEMNSSERE-----DCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 LVSQVTFNQNILVSASAPPDTSLRVWD 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 RVFRLQFDEFQIVSSS--HDDTILIWD 545
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                                                                                                                                                                                                                                                                                                                                                       NTGEMLNTLIHHCEAVLHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA 392
                                                                                                                              SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKVWDLVAALD 502
                                                                                                                                                                                     VWSVTFSPVTDDRPLLLASSSADQHIKLWDVATGKCLKTLKGHTREVHSVSFSPDGQTLA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQKIYSGLRDNTIKIWDKNTLECKRILTGHTGSYLCLQY--DERVIITGSSDSTVRVWDV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQIQERLILEPVKQKLLNIFGTELELHLRRMLGTLQKEPLPKKGYAAGNLINLLRQLQLD 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.6%; Score 413.5; DB 2 23.9%; Pred. No. 1.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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J. Mol. Biol. 195, 233-245, 1987

A:Title: Structural comparison of the yeast cell division cycle gene CDC4 and a relat A:Reference number: A26867; MUID:88011240; PMID:3309335

A:Accession: A26867
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A; Residues: 1-459, 'E', 461-779 <YOC>
A; Cross-references: EMBL:X05625; NID:g3502; PIDN:CAA29113.1; PID:g3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: initiation of DNA replication; C; Superfamily: unassigned WD repeat proteins; C; Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;628-659/Domain: WD repeat homology <WD2>
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-779 < MUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, April 1994 A; Reference number: 862302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: SGD:S0001885; MIPS:YFL009w
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A: Residues: 1-579 <CHU>
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A; Residues: 1-779 < MUR>
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submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces
A;Reference number: S56186
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C;Accession: 856245; $48310; A26867; $62304
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277 DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                         332 NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                             226 APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                          295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV-----
                                                                                                                                                                                                                     169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                            245 -----EISLKIFNYLQFED 294
                                                                                                                                                                                                                                                                                                                                                                                      194 TTPLAKTTKTINN------NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK-- 244
                                                                                                                                                                                                                                                                                                                                109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                          56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW 108
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Similarity 24.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 399; DB 2;
Pred. No. 9.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196; Indels 156;
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                                                                                                                                                                    -----SPKGF 331
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A:CLOSS TELEFELICES: EMBL:AFUJUSDO!; PLIN:AABJ948U.1 A:EXPERIBENTAL SUCRE: STRAIN h 972 R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. Submitted to the EMBL Data Library, August 1996 A; Recession: T38794 A; Recession: T38794 A; Recession: T98794 A; Rocession: DNA A; Reparlmental source: strain 972h; cosmid c4D7 A; Cross-references: EMBL:Z98602; PIDN:CAB11275.1; GSPDB:GN00066; SPDB:SPAC4D7.03 A; Experimental source: strain 972h; cosmid c4D7 R; Jallapalli, P.V.; Tien, D.; Kelly, T.J. R; Jallapalli, P.V.; Tien, D.; Kelly, T.J. R; Jallapalli, P.V.; Tien, D.; Kelly, T.J. R; Accession: T43798 A; Reference number: Z22686; MUID:98318628; PMID:9653157 A; Accession: T43798 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Kolecule type: DNA A; Residues: 1703 AJAL> A; Residues: 170	b 392 DNYVITGADDKMIRVYDSINKKFILL b 392 DNYVITGADDKMIRVYDSINKKFILL y 336 TGEMLNTLIHHCEAVLHLRFNNGMM b 452 KG
RESULT 14 A12493 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: A12493 R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T; Sasamoto, S; Watanabe, A.; Irigu Nakazaki, N; Shimpo, S; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MGID:2159285; PMID:11759840 A;Accession: A12493 A;Status: preliminary A;Accession: A12493 A;Status: preliminary A;Accession: A12493 A;Cross-references: GB:BA000020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene a177129 A;Genome: plasmid Query Match Best Local Similarity 26.7%; Pred. No. 6.50-21; Matches 96; Conservative 63; Mismatches 107; Indels 93; Gaps 10; Oy 280 IVSGLEDNTIKIMDKNILECKRILTGHTGSUCLOVDERVITGSSDSTVRVMDVNTG 337 I;	OY 60 ASTAMKTENCVAKTKLANGTSSMIVPKORKLSASYEK-EKELCVKYFEDGWSESDQVEFVE 118 155 NSISSNSDMPPPSPKYDTSNTVSPGSKPISEDLEDLINGSIVQFFEDLPGGIO-STAF 211 109 119 HLISONCHYOHGH-INSYLAPAGLDITAENILSYLDAKSLCAAELVCK 177 11

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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Pana Res. 8, 205-213, 2001
A; Tritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Resion: AC1842
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1747 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C:Genetics:
A; Gene: a110283
Search completed: February 20, 2003, 09:55:48 Job time: 28 secs
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 30-Jun-2002
C;Accession: AC1842
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                                                                                                                                                                                                                                               1663 ADNTIKLWNLPNATLLKTLLGHPGKINTLAFSPDGKTLLSGGEDAGVMVWNL--DLDDLM 1720
                                                                                                                                                                                                                                                                                                                                                                    1603 AIASVKFSPDSHTLASASWDNTIKLWQVTDGKLINNLNGHIDGVTSLSFSPDGEILASGS 1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1487 DGKTIATASADNTIKLWDSQTQQLIKTLTGHKDRITTLSFHPDNQTIASGSADKTIKIWR 1546
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                                                                                                                                                                                     506 PAGTLCLRTLVEHSGRV 522
                                                                                                                                                                                                                                                                                                      448 SDNTIRLWDIECGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKVWDLVAALDPRA 505
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Minimum DB seq length: 0
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Perfect score:
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SUMMARIES

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                                    541 GAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAG
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                                                                                                  CCTATGTTGCAGAGAGTTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCT
                                                                                                                                                       GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA
                                                                                                                                                                            GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA 480
                                                                             CCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGGATTGGATCATATCGCT
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NAT SANTE RECH MED (FR); KROLL MATHIAS (FR); DURAND HERVE (FR);
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//Protein_id="CaC07740.1"
//BL_xref="GI:100A3428"
//Translation="MDPAEAVLOEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
NSCARLCLNGETVCLASTAMKTENCYAATKLANGTSSNIVPKQRKLSASYEKEKELCY
KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALEARGLDHIAENI
LSYLDAKSLCAAEIVCKEWYRVTSDCMLWKKLIERWRTDSLWRGLAERRGWGQYLFK
NKPPDGNAPPNSEYRALYPKIIQDIETIESNWRCGRHSLQRHCRSETSKGVYCLQYDE
DQKIVSGLRDNTIKIWDKNTLECKTRLTGHTGSVLCLQYDERVITTGSSDSTYRVMYD
DQKIVSGLRDNTIKIWDKNTLECKTLITGHTGSVLCLQYDERVITTGSSDSTYRVMYD
VNVDDFDDKYIVSASGDRTIKVWNTSTGEFVETLNGHKRGIACLQYBDRLVYSGSSNN
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Zhang, H., Tsvetkov, L.M. and Kondo, T.
Modulation of protein levels using the
Patent: WO 0075184-A 42 14-DEC-2000;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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10 F-box protein FbwlA (FBWIA) mRNA,
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                AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
                                                                                      GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA
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AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG
                                                                    GGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAA
                                                                                                                                         TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chiaur, D.S. and Pagano, M. Direct Submission
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VNVVDFDDKYIVSASGDRTIKVWNTSTCEEVRTLNGHKRGIACLQYRDBLVVSGSSDN
TIRLWDIEGGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MDPAEAVLQEKALKFMNSSEREDCNNGEDPRKIIPEKNSLRQTY NSCARLCLNOETVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCV KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFTTALPARGLDHIAENI LSYLDAKSLCAAELVCKEWYRVTSOEMLWKKLLERMVETDSLWRGLAERRGWGQYLFK NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHGRSETSKGVYCLQYD NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHGRSETSKGVYCLQYD OQKIVSGLRDWIITGSSDSTYRWWDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="F-box protein Fbw1A"
/protein_id="AAF04464.1"
/db_xref="GI:6164610"
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70. .1779
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                                                                                                             Homo sapiens mRNA for beta-transducin 114153
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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FEATURES REFERENCE AUTHORS TITLE JOURNAL JOURNAL MEDLINE PUBMED source 1 (bases 1 to 2151)

Margottin, F., Bour, S.P., Durand, H., Selig, L., Benichou, S., Richard, V., Thomas, D., Strebel, K. and Benarous, R. A novel human WD protein, h-beta TrCp, that interacts with Vpu connects CD4 to the ER degradation pathway through an importif Submitted (03-JUL-1997) Finteractions Proteigues, Direct Submission Benarous, R. Paris, 9660940 98325370 (bases 1 to Cell 1 (4), 565-574 (1998) FRANCE /organism="Homo Location/Qualifiers . 2151 2151) æ . CHU sapiens" Benarous, Cochin, INSERM -24 rue de I.C.G.M., Labor de Fg.St-Jacques, Laboratoire

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NKPPDGNAPPNGFYRALYPKITOD IETIESNWRCGRHSLQAFIHCRSETSKYCLQYD
DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSYLCLQYDERVIITGSSDSTVEVWDV
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VNVVDFDDKYIVSASGDRTIKVMNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
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/protein_id="CAA74572.1"
/protein_id="CAA74572.1"
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/KTANSLATION="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
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70. 1779
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70. .1779
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/cell_line="Jurkat T-cell"
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TGATCCAGCTGCCCAAGCTGAACCCCCC 1740	GATGACACAATCCTCATCTGGGAC	1681	Qy
ATGAATTCCAGATTGTCAGTAGTTCACAT 1680	CATTCCGGAAGAGTTTTTCGACT	6	Db
GAATTCCAGATTGTCAGTAGTTCACA	ATTCCGGAAGAGTTTTCGAC		Qy
GACACTCTGTCTACGGACCCTTGTGGAG 1620	GTGGCTGCTTTGGACCCCCGTGC	1561 1561	Db Qy
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CATCAGGAATTGGTGCGTTGTATTCGA 15 	AATGTGGTGCATGTTTACGA		, DB 25
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CANCORACTECTETICAATGTTGTAGAC 12 	TTGATGACAAGTACATTGTTT	1201	Oy Cy
CATTGCTGTATGGGATATGGCCTCCCA 120 CATTGCTGTATGGGATATGGCCTCCCA 120 CATTGCTGTATGGGATATGGCCTCCCCA 120	GUCATGATGGTGACCTGCTCCA	ہ نہ د	9d 4d
AGCAGT AGCAGT	AAATGCTAAACACGTTGATTC	0 0	dd ;
ACGGTCAGAGTGTGGGATGTAAATACAGGT 1080 	AGTGATCATAAC <i>P</i> AGTGATCATAAC <i>P</i>	1021	DB QY
GTTCAGTCCTCTGTCTCCAGTATGATGAG 1020 	GAATGCAAGCGAATTCTCACAGG	961 961	Оy
CAATCAAGATCTGGGATAAAAACACATTG 960 	CAGAAAATAGTAAGCGGCCTTC	901 901	ОУ
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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IMAGE:5180993, mRNA, complete cds.
                                                                    Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                             Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 TTTATGAATTCCTCAGAGAGAGAGAAGACTGTAATAATGGCGAACCCCCCTAGGAAGATAATA 171
                                                                                                                                                                                                                                                                                                                    472 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352
                                                                                                                                                              608 CATATTGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                         412 GAATTTGTGGAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                                                                                                                                                  532 CATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTT
                                                                                                                                                                                                                                                                      548 TATCTTAAACCTATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGAT
          652 AGAATGGTCAGGACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAG
                                                                                                               592 GTGTGCAAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAG
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                                                                                                                                                                                                                                                                                                                                                                        GAATTTGTGGAACATCTTATATCCCCAAATGTGTCATTACCAACATGGGCACATAAACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAGAAGAATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAAGGAAAAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGCCAATGGCACTTCCAGTATGATTGTGCCCCAAGCAACGGAAACTCTCAGCAAGCTAT 351
                                                            Series: IRAK Plate: 62 Row: e Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 450:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 719
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NGMMVTCSKDBSIAVWDMASPTDITLRRVLVGHRAAVRVDFDDKYIVSASGDRTIKV
WNTSTCEFVRFLNGHRGIACLQYRDBLVYSGSSDNYITKMDLECGACLTAVLEGHEEL
VRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MDPAEAVLQEKALKFMCSMPRSLWLGCSSLADSMPSLRCLYNPG TGALTAFQNSSEREDCNNGEEPPRKIIPEKNSLRQTYNSCARLCLUQETYCLASTAMKT ERGYAKTKLANGTSSMYPKQFKKISASYEKEKELCVKFEGWSESDQVEFVEHLISQM CHYQHGHINSYLKPMLQRDFTTALPARGLDHLAENILSYLDAKSLCAAELCVKEWMYRY TSDGMLMKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNIKIWDKNTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="beta-transducin repeat containing"
/protein_id="AAB27994.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_lib="NHH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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/db_xref="LocusID:8945"
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                                                                                                                              CTTGTGGAGCATTCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGT
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                                                                                                                                                                                                         TGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2175)
1 (bases 1 to 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hatakeyama, S. and Nakayama, K.-i. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquitin dependent degradation of IkappaBalpha is mediated by ubiquitin ligase Skp1/Cul 1/F-box protein FWD1 Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3859-3863 (1999)
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NSCARLCINQETVCLTSTAMKTENCVAKAKLANGTSSMIVPKORKLSASYEKEKELCV
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LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLMRGLAERRGMGQYLFK
NKPDDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLORHURGETSKGVYCLOY
NOKIVSGLRDNTIKINDKSTLECKRILTGHTGSVLCLOYDERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHLRFINGMMVTCSKDRSIAVWDMASPDJTLRKYLVGHRAA
TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLMAALDPRAPAG
                                 VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1818 bp mRNA line Homo sapiens b-TRCP variant E3RS-IkappaB mRNA, AF101784
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TGALTAFONGSEREDCHNGEPPRKIIFDKNSLRQTYNSGARLCLNQETYCLASTAMKT
ENCVARTKLANGTSSMILVPKORKLSASTEKEKERLCVKYFEOWSESDQVEFVEHLISQM
CHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV
TSDGMLMKKLIEMVRTDSLWRGLAERRGWGYLFKNKPPDGNAPPNSFYRALYPKII
QDIETIESNMPGGRHSLGAIHGRSETSRGWGYLLGYDDKIYSGLADNIIKIMDKNTLE
CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCBAVLHLREN
NGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVVDFDDKYIVSASGDRFIKV
WNTSTCEFVRTLNGHKRGIACLQYNDRLVYSGSSDNTIHLWDLEGGACLRVLBGHEEL
VRCIREDNKRIVSGAXDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVERLQFDEF
UTSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTYISR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="b-TRCP variant E3RS-IkappaB"
/protein_id="AAD08702.1"
/db_xref="GI:4165136"
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receptor component of [KappaBa-ubiquitin ligase; contains
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94
Web site:
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                           This
                                                                                                                                           Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: o Column: 21
                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ed the following selection criteria: matched mRNA gi: 6753209
               /db_xref="taxon:10090"
/map="CZECH II"
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                      AACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAA 603
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                                                                                              TGGTACCGCGTGACGTCGGACGGCATGCTGGGAAAAAGCTCATCGAGAGGATGGTCAGG
                                                                                                                                                                                                         AACATTCTGTCATACTTGGACGCCAAGTCACTGTGTGCTGCTGAGCTCGTGTGCAAGGAA
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/db_xref="LocusII:12234"
/translation="MDPAEAPUQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTV
/translation="MDPAEAPUQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTV
/KYEDWSESDOVEFVEHLISOMCHYOHGHINSYLKPMLQRDEITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERWVRTDSLWRGLAERRGWGQYLFK
NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKVTCLQVDV
DQKIVSGLRDNTIKIMDKSTLECKRILTGHTGSVLCLQVDERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHLRENNGMMYTCSKDRSIAVWDMASDTDITLRRVLVGHRAA
VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVSGSSDN
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/protein_id="AAH03989.1"
/db_xref="G1:13278340"
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TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
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GACACAATTCTCATCTGGGACTTCCTGAATGATCCAGCTGCTCACGCTGAACCGCCCCGC
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One Baylor Plaza, Houston, TX 77030, USA
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  Conservative
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/product="beta-transducin repeat-containing protein"
/protein_id="AAD41025.1".
/protein_id="AAD41025.1".
/db_xref="di=5230822"
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLROTY
NSCARLCINQETVCLISTAMKTENCYAKAKLANGTSSMIVPKQRKLSASYEKEKELCV
KYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKADGTTTALPARGIDHITENI
LSYLDAKSLCAAELVCKEWYRVTSDGHLWKKLLERMVRTDSLWRGLAERGWGQYLFK
NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSGGYYCLQYD
DQKIVGSLDXTIHCEAVLHLRENNGMMVTCSXDRSIAVNDMASPTDITLRRVLVGHRAA
NAGBHLDTLTHHCEAVLHLRENNGMMVTCSXDRSIAVNDMASPTDITLRRVLVGHRAA
NAGBHLDTLTHHCEAVLHLRENNGMMVTCSXDRSIAVNDMASPTDITLRRVLVGHRAA
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                                                                                                                                    VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
TIRLMDIECGACLRVLEGHEELVRCIRFDNKRIVSGRYDGKIKVWDLMAALDPRAPAG
TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .1979
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                   72.9%;
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                 Score 1567.2;
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ATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTA 1089
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Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                    Craniata; Vertebrata; Sciurognathi; Muridae;
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B mRNA,
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Spencer,E., Jiang,J. and Chen,Z.J.
Signal-induced ubiquitination of IkappaBalpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                               Similarity
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
                                                                                                                                                               þ
                                                                                                                                                                                                                                                                                                                                                                                                                         /function="ubiquitinates phosphorylated IkBa"
/note="beta-TrCP; F-box protein; IkB-ubiquitin ligase;
substrate recognition subunit of SCF complex; similar to
Homo sapiens beta-TrCP and Drosophila melanogaster Slimb"
                                                                                                                                                                                                                                                                                                                          /product="beta-transducin repeat containing protein"
/protein_id="AAN04181.1"
/db_xref="G1:4140718"
/tdb_xref="G1:4140718"
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
/translation="MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY
NSCARLCINGETYCLTSTAMKTENCVAKAKLANGTSSMIYPKQRKLSASYEKEKELCV
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TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                                                                                                                                                                                                                                              DQKIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYGERVIITGSSDSTVRVWDV
NAGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA
                                                                                                                                                                                                                                                                                             KYFEQWSESDQVEFVEHLISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENI
LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                VNYVDEDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
                                                                                                                                                                                                                                                                             NKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                             score 1442.8;
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                                                     GTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATT 1209
                                                                                                    AACACATTGATTCACCACTGTGAAGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATG
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                                                                                                                                                                                                     Spevak, W., Keiper, B.D., Stratowa, C. and Castanon, M.J. Saccharomyces cerevisiae cdcl5 mutants arrested at a anaphase are rescued by Xenopus cDNAs encoding N-ras with beta-transducin repeats
Mol. Cell. Biol. 13 (8), 4953-4966 (1993)
                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.

1 (bases 1 to 1671)
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis
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Xenopus laevis (library: S. cerevisiae expression library
X.laevis occytes) cDNA to mRNA.
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M98268.1 GI:295542
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African clawed frog beta-TrCP
                              48. .1604
                                                                          oocytes"
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                                                                                                                                                     1. .1671
                                                                                                                                                                  Location/Qualifiers
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                                                                                  _lib="S. cerevisiae expression library of X.laevis
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                                                              GGGATAAGAATACTTTGGAGTGCAAGCGAGTGCTGATGGGTCACACTGGGTCAGTTCTCT
                                                                                                                                                                                                                                                                                                       GACTCGATCACATAGCAGAAAATATACTTTCATACCTGGATGCAAAGTCATTGTGTTCTG
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81.8%;
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GAYDGKIKWDLVAALDPRAPAGTLCLRTLYEHSGRVFRLQFDEFQIVSSSHDDTILI

0; Mismatches 262; Indels DB 5; Length 1671; 0, Gaps

284 AAACAAAACTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAG 343 0,

157 AGACAAAACTTGCCAATGGCACTTCCAGCATGATTGTGCCCAAGCAGCGAAAACTGTCAG 216

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396

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763

576 703

636

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GTCTGCAATATGATGAGAGAGTAATCATTACTGGCTCTTCAGACTCTACCGTCCGGGTGT GTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGT 106: 936

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTAAATGTGGTGGACTTTGATGACAAGTATATAGTCTCTGCATCTGGTGATCGAACAA 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2134 bp mRNA linear PRI 1. Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein beta-TRCP2 isoform A, complete cds.
                                                             Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center, Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan (E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402),
                                                                                                                                                                                                                                                                                                                                                                                                                \mathtt{BTRCP2}; \ \mathtt{F-box} and \mathtt{WD-repeats} protein beta-TRCP2 isoform Homo sapiens fetal lung cDNA to mRNA.
                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 269 (1), 103-109 (2000) 20160458
                                                                                                                                                                                                                                          Molecular cloning and genomic structure of the betaTRCP2 chromosome 5q35.1
                                                                                                                                                                                                                                                                                                       Koike, J., Sagara, N., Kirikoshi, H., Takagi, A., Miwa, T., Hirai, M. and
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                                               Fax:81-3-3541-2685)
                                                                                                                                    Direct Submission
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                             GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACA 957
                                                                                                                                                                                                                                                                                              TTCAAAAACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTAT 777
                                                                             TTGCAGAGGATTCAGTGCCGCTCTGAAAATAGTAAAAGGTGTCTACTGTTTACAGTACGAT
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/db_xref="G1:7209809"
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/translation="mepdsvledktielmisngtssvivsrkrpseggvgkekdlcik
/translation="mepdsvledktielmisngtssvivsrkrpseggldhiaenil
yedgwsesdgveevehllsrmchyghghlusvliserrgmdoytekn
yedgwsesdgveevehlisrmchyghghklierrgmdoytekn
yoldarsicaaelvckewgrvisegmlwkkliernwrdplwkciserrgmdoytekn
ryldarsicaaelvckewgrvisegmlwkkliernwcgrhuloriocreenskovycloyddek
rptdgppnsfyrslypkiigdietiesnwrcgrhuloriocreenskovycloyddek
IIsglrdnsikiwdktsledckyutghfcsvlcloydekvivtgssdstyrwwdvntg
evintlihhnerythlresuglavtcskdrslavwdmasatditerrulvghraavnv
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LWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLC
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Koike, J., Sagara, N., Kirikoshi, H., Takagi, A., Miwa, T., Hirai, M.
                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                             BTRCP2; {\tt F-box} and WD-repeats protein beta-TRCP2 isoform B Homo sapiens fetal lung cDNA to mRNA.
                                                                                                                                                                                                                    AB033280 2252 bp mRNA linear PRI 1 Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein
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         AAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATG
                                                                                                                                                                                                                                                                  AAGCCCATGTTGCAGCGGGACTTTATTACCGCTTTACCAGAGCAAGGCTTAGATCACATA 510
                                                AAAGAATGGCAGCGAGTGATCTCAGAAGGAATGCTTTGGAAGAAGCTGATTGAACGAATG
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Molecular cloning and genomic structure of the betaTRCP2 gene chromosome 5q35.1
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/VSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISMCHYQHGHINSYLKPML

QRDFITALPEQGLDHIAENILSYLDARSICAAELVCKEWQRVISEGMLWKKLIERMVR

TDPLWKGLSERRGWDQYLFKNNETDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQ

RIQCRSENSKGYYCLQYDDEKIISCHRONSIKUMDKTSLECLKVLTGHTSGVLCLQYD

RIQCRSENSKGYYCLQYDDEKIISHNDISHKUMDKTSLECLKVLTGHTSGVLCLQYD

BRVIVTGSSDSTVRVMDVNTGEVLNTLIHNEAVLHLRFSNGLMVTCSKDRSIAVMDM

ASATDITLRRVLVGHRAAVNVVDFDDKYLYSASGDRIKVTSTSCEFVFTLKGHKRG

IACLQYBDRLVVSGSSDNTIRLWDIEGGACLHVLGGHEELVRCIRFDNKRIVSGAYDG

KIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIMDFLN

VPPSAQNETRSPSRTYYISR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-OCT-1999) Masaru Katoh, National Cancer (Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104 (E-mail:mkatohénoc.go.jp, Tel:81-3-3542-2511(ex.4402), Fax:81-3-3541-2685)
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Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens fetal lung cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB033281.1 GI:7209812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     587
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA92331.1"
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TGHTGSVLCLQYDERVIYTGSSDSTVRYWDVPDEVLWTLHNERMLLHRESMGLMV
TCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTST
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FDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISS
SHDDTILIWDFLNVPDSAQNETRSPSRTYTYISR"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BTRCP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="5q35.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="fetal lung"
                                                                                                                                                                                                                                                                                                                                                        41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1768
                                                                                                                                                                                                                                                                                                                                                           Score 883.4; DB 9;
Pred. No. 2.3e-240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic structure of the betaTRCP2 gene
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein beta-TRCP2 isoform to mRNA.
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1617 1606	1558 CTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTG
1557 1546	1498 CGATITGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGAT
1497 1486	1438 ATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATT
1437 1426	1378 CAGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGAC
1377 1366	1318 ACAAGTACTIGTGAATTIGTAAGGACCTIAAATGGACACAAACGAGGCATIGCCIGTTIG
1317 1306	1258 GACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAAC
1257 1246	1198 CCAACTGACATTACCCTCCGGAGGGTGCTGGTCGACACCGAGCTGCTGTCAATGTTGTA
1197 1186	1138 AATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCC
1137 1126	1078 GGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAAT
1077 1066	1018 GAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACA
1017 1006	958 TIGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCCAGTATGAT
957 946	898 GATCAGAAAATGTAAGCGGCCTTCGAGACAACAATCAAGATCTGGGATAAAAACACA
897 886	838 TTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGAT
837 826	AAT TAT
777 、 766	718 TICAAAAACAACCTCCTGACGGGAATGCTCCCAACTCTTTTATAGAGCACTTTAT
717 712	658 GTCAGGACAGATTCTCTGTGGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTA
657 652	598 AAGGAATGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATG
597 592	538 GCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGC
532	473 AAGCCCATGTTGCAGCGGGACTTTATTACCGCTTTACCAGAGCAAGGCTTAGATCACATA

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